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Title:
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Maximum Match 100%
Listing first 45 summaries
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940
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	თ	o G	4	ω	2	_	Result
60.2	73:2	82.6	110.6	110.6	111	111	111.6	113.6	117.2	156	156	160.4	307.6	425.6	431.8	440.8	455.2	496.6	512.4	529.8	578	825.2	940	Score
6.4	7.8	8.8	11.8	11.8	11.8	11.8	11.9	12.1	12.5	16.6	16.6	17.1	32.7	45.3	45.9	46.9		52.8	54.5	56.4	61.5	87.8	100.0	Query Match Length
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Gabus-Parlix,C. and Darlix,J.
NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING PAtent: WO 9849334-A 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
LOCATION/Qualifiers
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/Strain="TYPE A (REV-A)"
/ISOLate="LEADER 5' DE L'ARN GENOMIQUE
/db_xref="taxon:11636"
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                                 2 (bases 1 to 4292)
Hertig,C.H., Coupar,B.E.H., Gould
Direct Submission
Submitted (30-MAY 1997) Division
                                                                                               1 (bases 1 to 4292)
Hertily.C., Coupar, B.E., Gould, A.R. and Boyle, D.B.
Field and yaccine strains of fowlpox virus carry integrated
sequences from the avian retrovirus, reticuloendotheliosis virus
Virology 235 (2), 367-376 (1997)
Portarlington Road, Geelong,
Location/Qualifiers
1. .4292
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                         Genbank staff at the National Library of Medicine Created this equence comes from Fig. 3.

Location/Qualifiers
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Filardo, E. J., Lee, M.F. and Humphries, E.H.
Structural genes, not the LTRs, are the primary determinants of 94279132
94279132
VIVOLOGY 202 (1), 116-128 (1994)
                                                                                                                                               Reticuloendotheliosis virus A.
Reticuloendotheliosis virus A.
Viruses; Retroid viruses; Retroviridae; Mammalian type
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/organism="Reticuloendotheliosis virus"
/db_xref="taxon:11636"
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423 uuuuuucuucuucuadauuggcagugagagagagauuuuguucgugguguaggcu 482

61 TTTTTTTCTTCTATATCCTCAGATTGGCAGTGAGAGAGATTTTGTTCGTGGTGTAGGCT 120

363 ggggucgccguccuacacauuguugugacgcgcgggcccagauucgaaucuguaauaaaag 422

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1 GGGTTCGCCGTCCTACACATTGTTGTGACGCGCGCGCCCAGATTCGAATCTGTAATAAAAG 60

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Location/Qualifiers
1. .583 Virus insertion. A attenuated strain JM-Hi3 reticuloendot Gallid herpesvirus 2
Viruses; dsDNA viruses, no RNA stage; Herpesviridae.
Isfort,R., Jones,D., Kost,R., Witter,R. and Kung,H.J.
Proc. Natl. Acad. Sci. U.S.A. 89 (3), 991-995 (1992) Gallid herpesvirus 2 attenuated strain JM-Hi3 reticuloendotheliosis \$79845

(REV IRR) [Marek disease virus, attenuated strain \$79845

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The control of the con S79845.1 GI:244514 /organism="Gallid herpesvirus 2" /insertion_seq="" 07-MAY-1993 1 JM-Hi3, , 583 ntj.

ce /organism="Spleen "" /organism="spleen "" /organism="spleen "" /db_xref="taxon:11836" /db_xref="cellular DNA" /ce /note="cellular DNA"	NE SE M	RESULT 6 REXXX1 REXX	Oy 480 geuggeeut [[::]: :	361 5 203 9 42 9 14	Db 383 Grand Canada Can	Db 19 CHILLIAN CAUCHING CATCARCACCATT TO CATAGACCACT TO CATAGACACT TO CATAGACT TO CATAGACACT TO CATAGACACT TO CATAGACT T	5 H W - B	C A	count 165 a 145 c	Tue Aug 8 08:33:17 2000
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M2224 M10660 M16722
M22224.1 GI:209709

long terminal repeat (LTR).
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                                                                                                                                                                                                                                 /note="cryptic intron 212 a 216 c 227 g About 700 bp after segment 1.
                                                                                                                                                                                                                                                                                                                                                        B-lymphoma induction by reticuloendotheliosis virus: Characterization of a mutated chicken syncytial virus involved in c-myc activation J. Virol. 61, 2084-2090 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 510 to 602)
Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J.
Ridgway,A.A., Swift,R.A., Kung,H.-J. and Fujita,D.J.
In vitro transcription analysis of the viral promoter involved compt activation in chicken B lymphomas: Detection and mapping two RNA initiation sites within the reticuloendotheliosis virus
                                                                                                                                                                                                                                                                                                                                                                                                             Swift, R.A., Boerkoel, C.F., Ridgway, A., Fujita, D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 3-Reticuloendotheliosis virus group.
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J. Virol. 54, 161-170 (1985)
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                                                                                                                                                                         45.9%; Score 431.8;
ilarity 66.8%; Pred. No. 1.7e
Conservative 137; Mismatches
                                     -ATCATTTCTCGGAATCGGCATCAAGAGCAGGCTCATAAACCATAAAAGG
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805. .806
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/db_xref="taxon:11636"
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O'Rear, J. J. and Temin, H.M.
Spontaneous changes in nucleotide sequence in provirus, necrosis virus, an avian retrovirus
Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-1234 (1982)
                                                                                                                                                                                                                                                                                                                                                                     1 (bases 2 to 470)
Shimotohno,K., Mizutani,S. and Temin,H.M.
Sequence of retrovirus provirus resembles that of bacterial transposable elements
Nature 285 (5766), 550-554 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     V01200 J02387
V01200.1 GI:61757
integration site; provirus; terminal repeat.
Spleen necrosis virus
Spleen necrosis virus
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/db_xref="taxon:11836"
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/note="T is
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LEWPTEGVGWPKEGTLDFKVVAAVRNITVFGNPGHPDQVTYITVMTDITLERFKYLKSC
GCKPHRTSKVLLASQKVWDRRFVLPSAFESPFRITRAQFLDERPLSPAFAPPPFYPEV
SALVEDTREGQOPDSTVMTSPPHTRSGLEFGAGDFSGWYPLRETGERDWTTYV
PFTTSDLYNWKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER
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/note="A is T in clone
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/protein_id="CAA24513.1"
/db_xref="GI:61758"
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Pred. No. 1.7e-124;
60; Mismatches 29;
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Spleen necrosis virus
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Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 1-Mammalian type C virus group.
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/organism="Spleen necrosis virus"
/ob_xref="taxon:11836"
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Matches 140; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-MAY-1997) Division of Animal Health, CSIRO, Portarlington Road, Geelong, Victoria 3213, Australia Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 1022)

Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.

Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virus virology 235 (2), 367-376 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hertig, C.H., Coupa
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF006066 1022 bp DNA VRL Fowlpox virus S envelope glycoprotein (env) gene, 3'_long_terminal repeat, complete sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Avipoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fowlpox virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AF006066.1 GI:2393896
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                                                                                                315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 1022)
                                                                               /product="putative protein"
/protein_id="AAC58242.1"
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DNNPV5LKTFTCPSKNSIRQFTKELDLLRSLQSSEHVIKLYGYILDI"
a 209 c 218 g 280 t
                                                                                                                                                                                                                                                                       /product="envelope glycoprotein"
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IARKRALYDNPLWNGLNGFLPYLLPLLGPLFGLILFLTLGPCISKTLTRIHAQKSGS
KNPSIOSPAVQATPNRDGYPRSMI"
                                                                                                                                                                                                                                                                                                                                                                                                   /gene=0
                                                                                                                                                                                                                       deletions in U3, R, been duplicated."
                                                                                                                                                                               /codon_start-1
                                                                                                                                                                                                note-"ORF1"
                                                                                                                                                                                                                                                                                                                                                                                                                                  /strain="S (Standard Vaccine strain)"
/db_xref="taxon:10261"
/note="standard vaccine strain from Cyanamid-Webster
Ltd. Castle Hill, New South Wales, Australia
integrated reticuloendotheliosis virus"
                                                                                                                                                                                                                                                                                                                                                                                     /gene-"env"
                                                                                                                                                                                                                                                                                                                                                                     /codon_start=2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Fowlpox virus"
/strain="S (Standard Vaccine strain)"
                     17.18;
64.28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coupar, B.E.H., Gould, A.R. and Boyle, D.
                                                                                                                                                                                                                                                                                                                                                                                                              env"
                                                                                                                                                                                                                             LTR of reticuloendotheliosis provirus; LTR has in U3, R, U5 regions; first 23 bp of U3 have
       53;
   Score 160.4; DB 82
Pred. No. 6.8e-40;
3; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              537
                            82;
    Indels
                              Length 1022;
   19;
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partial cds
 Gaps
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AF006064
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181 gaaauguucguuggaggcgagcaucagaccacuugcgc 218
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Hertig,C.H., Coupar,B.E.H., Gould,A.R. and Boyle,D.
Direct Submission
Submitted (30-MAY-1997) Division of Animal Health,
Portarlington Road, Geelong, Victoria 3213, Austral
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis v Virology 235 (2), 367-376 (1997)
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Hertig,C., Coupar,B.E.,
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Fowlpox virus M long
kinase homolog gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Avipoxvirus.
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CLEGSCTVNVBLGDRQISDNISESSGFLMDVNTDHVLDTKYVGLFITKIKVDAHVFYG
ONVIMFPEKNLFSQTNGPNFILYDITYODRNVLLLITSKYITNLCDDKYYDIFELKYL
VDNCKLPMPLIPLSKYDFTFTDLSVIKSENVKTVLSKVHTSNKSYYNNDTSLPVAVKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .2640
/Organism="Fowlpox virus"
/Strain="M (mild vaccine strain)"
/Sb_xref="taxon:10261"
/note="mild vaccine strain from Cyanamid-Webster
__actie_Hill, New South Wales, Australia.
                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                  'note-"remnant of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note-"ORF1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA VRL 16-SEP-1997 terminal repeat, complete sequence, protein complete cds, and serpin gene, partial cds.
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                                                                                                                                                                                                                        reticuloendotheliosis virus"
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Matches 137
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGAGGGAGCTCCGGGGGGAATAGCGCTGGCTCGCTAACTGCCATATTAGCTTCTGTAATC 967
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ggagggagcuccggggggaauagcgcuggcucgcuaacugccauauuagcuucuguaauc 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
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AF198100
                                                                                                                                                                                                                                                                                                                                                                    Fowlpox virus
Viruses; dsDNA viruses,
                                                                                                                                                                                                                                                                                                                                                                                                                          AF198100.1 GI:7271507
                                                                                                                                                                                  Submitted (24-OCT-1999) Microbiology, Plum Island Animal Disease Center, U.S. Dept. Agriculture, Agricultural Research Service, P.O. Box 848, Greenport, NY 11944-0848, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                              1 (bases 1 to 288539)
Afonso,C.L., Tulman,E.R., Lu,Z., Zsak,L.,
The genome of fowlpox virus
J. Virol. 74 (8), 3815-3831 (2000)
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2116. .>264
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IPRIMNKWIRSRSNNKITDIGCHIYDNTKSIIAEAMFFTMKHESIFGSTRKDTITFYK
YDGTSLPVEAIHADP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NMDYQGIYNMLIKENKGEYMPLDCPLELQCIVIACRNTNSIFRPSISAIIDFLETFYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="ORF3"
                                         complement(1874. .2491)
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             complement(1874. .2491)
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                                                                                                 /note="virulent FPV; Fowlpox Challenge Virus"
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/country="USA: APHIS Center for Veterinary Biologics,
                                                                                                                                                       /organism="Fowlpox virus"
                                                                         /note="left end"
/note="C-type lectin gene family protein identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         288539 bp
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                                                                                        9520
                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete
                                                                                                                   Iowa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 156; DB 82;
Pred. No. 1.8e-38;
1; Mismatches 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     431 g
                                                                                                                                                                                                                                                                                                                                                                       no RNA stage; Poxviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           genome
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                                                                                                                                                                                                                                                                                                                                   Kutish, G.F.
                                                                                                                                                                                                                                                                                                                                                                               Chordopoxvirinae;
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VGFRGGIOKCEKGSDMIGKSEEEMKALKNITGKODESFEWODNRAASTFDDVNECA
YGTRSSVSEVPKYUISPCSVRRYLVCKKTDNSYPTTQSSFYNQYE"
3367. 4035
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GB:AF021350"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAP44597.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="FPV002"
3367. .4035
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MKSLILIAMLLMLDCANSLNCRGPYTSYNNKCIWVNRLDKMHHK KTYSBASTTCLITEPMCTLARRSLIDNEKDMKFISKFGMGQSLWIRDDKKPEVGKCAY TDGKTFGFSPCNATYGFVCID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4500. .4871)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="FPV002"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="identical to FPV258 Fowlpox PIR:C31685 (vaccinia A40R), similar to Homo sapiens SW:Q07108"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="ORF FPV002 hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="identical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(4500.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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5931. 7187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MNNDTIFTLFYCKNKKYVRGEGGRRRGKTGILLFHPINHRVIGTSAHQCYKTRRIGFKLYAVAPRHVSTIRCGRSHSAHRVDKFSFSFQKVDFHCIAGSGA"
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/gene="FPV004"
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/gene="FPV005"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(522
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vnote="identical to FPV257 Fowlpox GB:A06621"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="FPV004"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ó
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                                                                                                                                                     gene
                                                                                                                                                     family protein"
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gene CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note="Fowlpox SW:P14369, similar to GB:AB006423"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(9123. .10190)
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Complement(9123. .10190)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /gene="FPV009"
8048. .824°
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="ORF FPV010 Serpin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F
7681. .8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="identical to FPV252 Fowlpox GB:D00295"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="FPV009"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   similar to Gallus
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="identical to FPV253 SW:P14370 (vaccinia A40R), similar to Gallus gallus GB:AB015628"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MLYSVETRIYKIRKNNKTEMILAIYDRNAYIVKKTGIGSILLRD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /681. 8184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     db_xref-
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BASE COUNT
                                                                                                                                                                                                        REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                            KEYWORDS
SOURCE
ORGANISM
                                                                                                                                    FEATURES
                                                                                                                                                                                                                                                                                                                       DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                                                                                                                                                                                             RESULT
SNVLTR
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Best Local S
Matches 137
                                  polyA_signal
                                                              misc_feature
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Iwasaki, K. and Temin, H.M.

The efficiency of RNA 3'-end formation is determined by the distance between the cap site and the poly(A) site in spleen necrosis virus
                                                                                                                                                                                                                                        Spleen necrosis virus
Spleen necrosis virus
Viruses; Retroid viruses;
retroviruses; 1-Mammalian
                                                                                                                                                                                                                                                                                                       LTR.
                                                                                                                                                                                                                                                                                                                                    spleen
X59450
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                         /note="LTR"
74..70
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                                                                                                                                                                                                                                                                                                                                          180 bp
necrosis virus
                                                                     /organism="Spleen necrosis virus"
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                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Translation-"MDTEMDGVNNDGYTSLYKETAKGNIKKTVELLYKGVNPNTPNVD SYTPLHIAAKTONIKIIRRLIBYGANVDKETNDGYTALLIAICTGDIKTCNVLLDEGA NPNYVNKYGITPLVRIISYTRTIIKLIBYGANVDKETNDGYTALLIAICTGDIKTCNVLLDEGA KIPILNIVPYIIISKTRASITVNIEGFNRNIAAIAKNSRLLEVALKCKSELAFMTTR GIGDKSLFEICILEDIKDIDHNSFVAFLDKLIESQSNLRIYGYTMNKIIEMGRYKREL CSSAVRVNSCNLSSLATEWCLLPLKGKLNILSKLNNDNIKKLILNDAIKVNNKTG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(13708. .13890)
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Pred. No. 2.5e-38;
1; Mismatches 5;
ω
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type C virus group.
 57
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Search completed: August 7, 2000, 10:53:33 Job time: 5987 sec
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12.5%; Score 117.2; DB 81; Length 180;
Best Local Similarity 61.0%; Pred. No. 3.7e-26;
Matches 94; Conservative 44; Mismatches 13; Indels 3; Gaps
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Page 12

	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd. Compugen Ltd. Seconds OM nucleic - nucleic search, using sw model OM nucleic - nucleic search, using sw model (without alignments) (without alignments) August 7, 2000, 09:13:47; Search time 205.61 Seconds (without alignments) August 7, 2000, 09:13:47; Search time 205.61 Seconds (without alignments)	us-09-214-124-1.rng . Tue Aug 8 08:33:18 2000
PRESULT 1 V63778 standard; DNA; 940 BP. V64778 standard; DNA	37 28.2 3.0 10000 1 X13948 Human II-1ra BAC C 28.2 3.0 11425 1 X13948 Human II-1ra BAC C 40 28 3.0 3412 1 Q51156 Human II-1ra BAC C 41 28 3.0 3412 1 X03046 Hereditary haemoch 42 28 3.0 2373 1 V57903 C 42 28 3.0 237033 1 V57903 C 43 28 3.0 237326 1 T07329 C 44 28 3.0 237326 Human calcium sign C 42 28 3.0 237326 Human calcium sign C 43 28 3.0 237326 Human calcium sign C 44 28 3.0 237326 Human calcium sign	28.2 3.0 947 1 T79933 28.2 3.0 3474 1 V99927 28.2 3.0 3789 1 Q44362 28.2 3.0 3789 1 T47716 28.2 3.0 9299 1 T67719

Page N

RESULT X26113
ID X26113
ID X26113
ID X261
ID X26
ID occurrence in chickens
The inventor relations to a recombinant fowlpox virus (FPV) whose nucleic vaccinated at older than 1 day of age. Alternatively, Chickens can be vaccinated with the vaccine subsequent to vaccinated at older than 1 day of age. Prior vaccine and field strains with the vaccine with the vaccine subsequent or vaccinated with the vaccine subsequent of vaccination with the vaccine subsequent of vaccination with the vaccine subsequent to vaccination with the vaccine subsequent of vaccination with the vaccine subsequent to vaccination with the 닭 Ą 18-FEB-1999. 07-AUG-1998; AU0628. 08-AUG-1997; AU-008454. В Recombinant vaccine against fowlpox virus - is free of contamination reticuloendotheliosis virus, used to prevent the virus (CSIR) CO Boyle DB, WPI; 99-16 ş В Ą 8 20-MAY-1999 (first entry)
FowLpox virus (FPV S) S' LTR sequence.
FowLpox virus; FPV; recombinant; reticulcendotheliosis virus; REV;
ROWLPOX virus.
10-MAY-1999 (first entry)
1 δÃ 멍 Ş Д δÃ Д X26113 standard; DNA; 4643 BP. Qy В δõ 901 guuuguacucguccuccuccucuccggccgggauggg 940 901 GUUUGUACUCGUCCCCCCCCCCCCCCGCCGGCCGGAUGGG 940 DЪ δÃ R) COMMONWEALTH SCI & IND RES ORG. 99 167428/14 BEH, Gould AR, Hertig C; 841 gcccacaccgcgcgccuugcgaauaauacuuuggagagucuuuugccuccagugucuucc 900 D, Ş 781 uguuuguuuguuuguuuguuuguuogucacuugucgacagcgcocugcgaauuggugu 840 В δ 721 ugguaucugauuguuggaccgucuccaagacggugauaauauaagucgugguuugug 780 661 cgggacgcugccggggaagcuccaccuccgcucagcagggggacgccugaucugagcucug 720 601 gcgccgguaaguacuugauuuugguaccucgcgaggguuugggaggaucggagugg 660 GCCCACACCGCGCGCGUGCGAAUAAUACUUUGGAGAGUCUUUGGCCUCCAGUGUCUUCC 541 GGGGGCUCGUCCGGGAUUCCCCCAUCGGCAGAAGUGCCUACUGUUUCUUCGAACUCCG 541 99999cucqucc9999auuccuccccaucggca9aagugccuacuguuucuucgaacuccg 600 481 cuggccuacugggugggguagggguccggacugaauccguaguauuucgauacaacauuu 540 uguuguuguakeeduguguuguuegueakeudgueakeakeedeedeakaauuguugu 481 CUGGCCUACUGGGGUGGGGUAGGGGUCCGGACUGAAUCCGUAGUAUUUCGAUACAACAUUU udenaucudanudenudenudenceducuccaaddegedanaanaanaddegedegenudagencedudend CGGGACGCUGCGGGAAGCUCCACCUCCGCUCAGCAGGGGGACGCCCUGAUCUGAGCUCUG 361 ucggggucgccguccuacacauuguugugacgcgggcccagauucgaaucuguaauaaa 420 GCGCCGGUAAGUAAGUACUUGAUUUUGGUACCUCGCGAGGGUUUGGGAAGGAUCGGAGUGG 301 301 aguuuuuuuucuucuucagauuggcagugagagagagauuuguucguggugagg 480 - GAAAAUGUCAUGCAACAUCCUGUCCUGUAAGCGGCUAUAUAAGCCAGGUGCAUCUCUUGC 360 9aaaaugucaugcaacauccuguccuguagcggcuauauaagccaggugcaucucuugc 360 ₽ Ş DЪ Š . B δÃ Д Ş 뮍 δÃ B Qγ В δÃ DЪ δÃ В Š

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The present sequence is derived from the 5' end of the genomic RNA of Reticuloendotheliosis virus type A (REV-A). The specification also describes nucleotide sequence derived from all or part of the 5' end of the genomic RNA of a type C retrovirus other than Friend murine leukaemia virus (FMLV) and Moloney murine leukaemia virus (MoMLV). The 5' derived sequences are used as an internal ribosome entry site (IRES) in a vector for permitting or enhancing the encapsidation of a retrovirus vector. The vectors can be used for gene therapy, production of recombinant polypeptides or production of transgenic animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-APR-1997; 005203.
28-APR-1997; FR-005203.
(INFM ) INSERM INST NAT SANTE & RECH DARLIX JL, GABUS DARLIX C, LOPEZ LM; WPI; 99-037487/04.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence derived from the 5' end of REV-A. Reticuloendotheliosis virus type A; REV-A; type C retrovirus; internal ribosome entry retroviral vector; gene therapy; ss. Reticuloendotheliosis virus.
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22-DEC-1994.
07-JUN-1994; U06415.
07-JUN-1993; US-073345.
(UYNE-) UNIV NEW JERSEY.
Dornburg RC;
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Similarity 63.4%;
94; Conservative 168
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Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and form provirus

Example: Page 17: 28pp; English.

The universal retroviral vector pPoll5-R1 (given in Q76041) was obtained by replacing the SV40 promoter and hpt gene of pPOll1-R1 (Q76038) with the multiple cloning site of pBluescript II KS. The vectors allow cell-type specific gene expression and eliminate ris of downstream activation of cellular proto-oncogenes.

Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T;
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Matches 362
                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccinated with the vaccine subsequent to vaccination with FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provitus of REV sequences. Some of the FPV strains carry when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chicken syncytial virus provirus REV LTR sequence. FOWLpox virus; FPV; recombinant; reticuloendotheliosis virus; vaccine; chicken; LTR; long terminal repeat; ss. Avian reticuloendotheliosis virus.
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Example 4; Fig 5; 127pp; English.
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07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
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Boyle DB, Coupar BEH, Gould AR, Hertig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Recombinant vaccine against fowlpox virus - is free of contamination from reticuloendotheliosis virus, used to prevent the virus
                                      243
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                                                                    standard; DNA; 512 BP
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                                                                                                                                                                                                                                                                                                                                                                  130 A;
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                                                                                                                                                                                                                                                                                              Score 436.2; DB 1;
Pred. No. 7.6e-139;
7; Mismatches 13;
                                                                                                                                                                                                                                                                                                                                                                    113 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ç
                                                                                                                                                                                                                                                                                                                                                                    129 G;
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                                                                                                                                                                                                                                                                                                                                                                    140 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CC contamination by Exp many sequences. Some of the FPV strains carry a near full length provides the means by which a FPV vaccine free from contamination by REV sequence. So sequence as a FPV LISURURE CONTAMINATION of REV. Sequence. The recombinant FPV is contained and sequence of the produce a vaccine against fowlpox virus. The vaccine is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day can be vaccine to vaccinated with the vaccine subsequent to vaccination with constrain at 1 day of age. Prior vaccine and field strains at 1 day of age. Prior vaccine and field strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The present invention provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences X26110-115 represent FPV long terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above.

So sequence 536 BP; 145 A; 115 C; 133 G; 143 T;
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 362; Conserv
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W09907852-A1.
18-FEB-1999.
07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
08-AUG-1997; AU-008454.
08-GUG-1997; AU-008454.
08-AUG-1997; AU-008454.
08-AUG-1997; AU-008454.
08-AUG-1997; AU-008454.
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20-MAY-1999 (first entry)
Fowlpox virus (FPV M5) LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis
vaccine; chicken; LTR; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Recombinant vaccine against fowlpox virus from reticuloendotheliosis virus, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (CSIR ) COMMONWEALTH SCI & Boyle DB, Coupar BEH, Gould WPI; 99-167428/14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X26110 standard; DNA; 536
X26110;
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                     46.3%; Score 435.4; DB 1; 67.9%; Pred. No. 1.5e-138; tive 135; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ВP
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                                                                                                                                                                                                                                                                                                                                                                                r Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect r host.cell and form provirus sexample; Page 13-14; 28pp; English.

New recombination-free, highly efficient retroviral vectors peolil-R1 (given in Q76038), peolil-R2 (Q76039) and peolil-R3 (Q76040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5528 BP; 1265 A; 1423 C; 1457 G; 1383 T;
                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 397; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-DEC-1994; 07-JUN-1994; 1
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WPI; 95-036467/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        long terminal repeat;
gene therapy; ss.
Spleen necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Retrovirus; vector; pPO111-R1; spleen necrosis virus; SN Retrovirus; vector; pPO111-R1; spleen necrosis virus; SN cytomegalovirus; CMV; intermediate-early promoter; IE promoter cytomegalovirus; CMV; intermediate-early gromoter; in promoter; in promoter; in promoter cytomegalovirus; cMV; intermediate-early promoter; in promoter; 
              509
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                                        cagugagagagaunuuguuguuguuguggugagcuacugggugg-guagggguccg
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US-073345.
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                                                                                                                                                                                                                                                                                                            45.88;
                                                                                                                                                                                                                                                                                              169;
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                                                                                                                                                                                                                                                                                       Score 430.4; DB 1;
Pred. No. 2.8e-136;
9; Mismatches 36;
                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                     Query Match
Best Local Sim
Matches 386;
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                                                                                                                                                                                                                                     ability to produce progeny virus, in helper cell which can infost cell and form provirus

Example; Page 14-16; 28p; English.

New recombination-free, highly efficient retroviral vectors
pPO111-R1 (given in Q76038), pp0111-R2 (Q76039) and pp0111-R3 (Q76040) were obtained by replacing the U3 region of the left
LTR of spleen necrosis virus with the IE promoter/enhancer of and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5525 BP; 1264 A; 1422 C; 1457 G; 1382 T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO9429437-A.
22-DEC-1994.
07-JUN-1994; 1
07-JUN-1993; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cytomegalovirus; proll1-R2; spleen necrosis virus; long terminal repeat; LTR; encapsidation; gene transfe gene therapy; ss. Spleen necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dornburg RC;
WPI; 95-036467/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant retrovirus vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q76039 standard;
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                                                                    ucucuugcucggggucgcguccuacacauuguu---gugacgcgcgggcccagauucgaa 409
ucuguaanaaaaguuuuuuucuucuaaneccucagauuggcagugagagagauuuuguu
                                         TCTCTTGCTCGGGGTCGCGTCCTGCACATTGTTGTTGTGACGTGCGGCCCAGATTCGAA 730
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; US-073345.
V NEW JERSEY.
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ector pPO111-R2.
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                                                                                                                                                            44.7%;
62.7%;
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                                                                                                                                     166;
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                                                                                                                                  Score 420; DB
Pred. No. 9.9e
56; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contg. non-retroviral
us, in helper cell whi
                                                                                                                                DB 1; I
).9e-133;
hes 30;
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                                                                                                                                                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 iral gene,
which can
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                                                                                                                                                                                                                                                                                                                                              gene therapy; ss.

Spleen necrosis virus.

W09429437-A.

W09429437-A.

22-DEC-1994.

22-DEC-1994.

07-UN-1994.

US-073345.

07-JUN-1993.

US-073345.
cell-type s
downstream
Sequence
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Q76040;
                                                                                             pornburg RC;
WPI; 95-036467/05.
Recombinant retrovirus vector, contg. non-retroviral gene, - h
Recombinant retrovirus vector, contg. non-retroviral gene, - h
Recombinant retrovirus virus, in helper cell which can inf
ability to produce progeny virus, in helper cell which can inf
host cell and form provirus
Example; Page 16-17; 28pp; English.
Example; Page 16-17; 28pp; English.
New recombination-free, highly efficient retroviral vectors
pP0111-R1 (given in Q76038), pP0111-R2 (Q76039) and pP0111-R3
(Q76040) were obtained by replacing the U3 region of the left
LTR of spleen necrosis virus with the IE promoter/enhancer of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1995 (first entry). Retrovirus vector pPO111-R3. Retrovirus; vector; pPO111-R3; spleen necrosis virus; SN Retrovirus; vector; pPO111-R3; spleen necrosis virus; SN cytomegalovirus; CMV; intermediate-early promoter; IE pr long terminal repeat; LTR; encapsidation; gene transfer;
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     extension of the encapsidation region. The vectors 1-type specific gene expression and eliminate risks constream activation of cellular proto-oncogenes. pence 5519 BP: 1264 A; 1420 C; 1456 G;
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Matches
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20-MAY-1999
                                                                                                                                                                                                                                   1270
                                                                           18-FEB-1999.
07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
(CSIR ) COMMONWEALTH SCI & IND RES ORG BOYle DB, Coupar BEH, Gould AR, Hertig WPI; 99-167428/14.
                                                                                                                                              20-MAY-1999 (first entry)
FOWIPOX virus (FPV S3') LTR sequence.
FOWIPOX virus; FPV; recombinant; reticuloendotheliosis virus;
vaccine; chicken; LTR; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                     1150
occurrence in chickens; claim 18; Fig 5; 127pp; English. Claim 18; Fig 5; 127pp; English. The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (RBV), and whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be
                                                                                                                             Fowlpox virus. W09907852-A1.
                                                           Recombinant vaccine against fowlpox virus from reticuloendotheliosis virus, used to
                                                                                                                                                                                        X26111 standard; DNA;
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OL COLORD SERVICE SERV
PT occurrence in chickens

Staim 18; Fig 6; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and to whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be contained at older than 1 day of age. Alternatively, chickens older than 1 day of age. Alternatively, chickens older than 1 day of age. Prior vaccination with the vaccinated with the vaccine subsequent to vaccination with the province of FPV M (FPV mild strain) at 1 day of age. Prior vaccine and field strains come of FPV carry integrated REV sequences. Some of the FPV strains carry a come trull length provirus of REV, and can give rise to infected. The containation by REV may be produced. Sequences are infected. The containation by REV may be produced. Sequences x26110-115 represent FPV conjugated to the containation by REV may be produced. Sequences x26110-115 represent FPV conjugated contains a first sequences. The new recombinant FPV nucleic acid conjugated co
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Best Local S
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18-FEB-1999.
07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CSIR ) COMMONWEALTH SCI & IND RES ORG. Boyle DB, Coupar BEH, Gould AR, Hertig WPI; 99-167428/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Recombinant vaccine against fowlpox virus from reticuloendotheliosis virus, used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fowlpox virus (FPV S) 3' LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
vaccine; chicken; LTR; long terminal repeat; ss.
Fowlpox virus.
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Fowlpox virus (FPV S) 3' I
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X26115;
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nes 140; Conservative
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Pred. No. 6.3
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    is free of contamination
prevent the virus

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Score 160.4;

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Statum 18; Fig 5; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic acid does not encode an active reticuloendotheliosis virus (REV), and CC whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to compare the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than 1 day of age. Alternatively, chickens older than 1 day of age. Prior vaccine and field strains car y and the vaccine subsequent to vaccination with the vaccine subsequent to vaccination with the vaccine for vaccine and field strains carry a compared to the province of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent FPV contamination by REV may be produced. Sequences x26110-115 represent
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Best Local S
Matches 137
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07-AUG-1998; AUG628.
08-AUG-1997; AU-008454.
(CSIR) COMMONWEALTH SCI & IND RES ORG.
EOYLE DB, COUPAR BEH, Gould AR, Hertig
WPI; 99-167428/14.
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FOWLpox virus (FPV M3) LTR sequence.
FOWLpox virus; FPV; recombinant; reticuloendotheliosis virus;
vaccine; chicken; LTR; long terminal repeat; ss.
FOWLpox virus.
FOWLpox virus.
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nes 137; Conser
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        aucggcaucauuucucggaaucggcaucaagagcaggcucauagaccauaaaaggaaaug
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                                                                                                                                                                                                                                            Score 156; DB 1;
Pred. No. 2e-43;
1; Mismatches
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    is free of cont
prevent the virus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a recombinant fowlpox virus (FPV) whose nucleic caid does not encode an active reticuloendotheliosis virus (REV), and CC whose genome does not contain any REV sequence. The recombinant FPV is CC used to produce a vaccine against fowlpox virus. The vaccine is used to produce a vaccine against fowlpox virus. The vaccine is used to cC prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens older than CC 1 day can be vaccinated with the vaccine subsequent to vaccination with CC 1 day can be vaccinated with the vaccine subsequent to vaccination with CC of FPV mild strain) at 1 day of age. Prior vaccine and field strains CC of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV CC when transfected into cell cultures and when chickens are infected. The CC contamination by REV may be produced. Sequences x26110-115 represent FPV clong terminal repeat sequences. The new recombinant FPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above.

SQ Sequence 1100 BP; 392 A; 177 C; 196 G; 335 T;
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Best Local Similarity
Matches 137; Conser
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07-AUG-1998; AU0628.
08-AUG-1997; AU-008454.
(CSIR) COMMONWEALTH SCI & IND RES
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Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus;
vaccine; chicken; LTR; long terminal repeat; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     occurrence in chickens
Claim 18; Fig 6; 127pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant vaccine against fowlpox virus - is free of contamination from reticuloendotheliosis virus, used to prevent the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Boyle DB, Coupar BEH, Gould WPI; 99-167428/14.
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      Phaseolus lunatus
                                  Phaseolus lunatus; ADA2; transcription
                                                            Phaseolus lunatus ADA2 transcription adapter encoding cDNA.
                                                                                                 12-MAY-1999 (first entry)
                                                                                                                                                    X18925 standard; cDNA; 1812
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TTTGTTGAAGGCAAGCATCAGACCACTTGCAC
                                                                                                                                                                                                                                                                                                  augcuugcuugccuuagccgccauuguacuugauauauuucgcugauaucauuucucgga 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 11|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1|| | 1||
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Pred. No. 4.2e
51; Mismatches
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                                         adapter;
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1.2e-43;
nes 5;
                                         herbicide;
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New isolated nucleic acid encoding plant ADA2 transcription activator - used for regulating expression of genes in plants and to pr activator - used for regulating expression of genes in plants and to present screen for specific inhibitors, potentially useful as herbicides claim 2; page 26-28; 40pp; English.

Claim 2; page 26-28; 40pp; English.

CC price present sequence encodes the ADA2 transcription adapter isolated crown phaseolus lunatus. Also described are chimeric genes comprising compensor that the expression operably linked to suitable regulatory the ADA2 nucleic acid sequence operably linked to suitable regulatory comparticularly to reduce expression of particular genes can be used: (i) to compare the expression of particular genes whose promoters care normally regulated by ADA2, using antisense or co-suppression compared by factors with which ADA2 interact; and (ii) to compounds that inhibit ADA2, potentially useful as herbicides. Fragments of the ADA2 nucleic acid sequence (or synthetic primers based on it) are used in hybridisation screens to obtain sequences encoding homologous sequences from other plant genomic libraries, also for mutant phenotypes.

Sequence 1812 BP; 613 A; 318 C; 404 G; 477 T;
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V74552
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Matches 45
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15-JUL-1998; U14904.
18-JUL-1997; US-897175.
(DUPO ) DU PONT DE NEMOURS
                                                                                                                                                                                                                                    Staphylococcus aureus contig SEQ ID #241.
Computer readable medium; vaccine; S.aureus infection; immunodetection; cellulitis; eyelid infection; food poisoning; osteomyelitis; therapy; skin infection; surgical wound infection; scalded skin syndrome;
                                                                                                                                                                                                                                                                                                        V74552;
16-MAR-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                           V74552
                                                                     misc_feature
                                                                                                                                                                                                    Staphylococcus
                                                                                                                                                                                                                      toxic shock syndrome; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                             433
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45; Conser
                                                                                                                                                                                                                                                                                                                                         standard; DNA; 5000
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the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence"
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Pred. No. 0.49;
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Pr Polynucleotide(s) and proteins derived from Staphylococcus aureus - Pr stored on computer readable medium and used in the production of Pr anti-S.aureus vaccines
PS Claim 1: Page 1025-1028; 3271pp; English.
CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences
CC of the invention. The DNA sequences are recorded on a computer readable
CC medium, preferably selected from a floppy or hard disk, random access
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC that protein-encoding or regulatory regions of commercial, therapeutic or
CC likely to encode antigens have been identified and these polypeptides can
CC be used in a vaccine composition against S.aureus infection. The
CC saureus in a sample. S.aureus is implicated in numcrous human diseases,
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC skin and surgical wound infections, scalded skin syndrome, toxic shock
CC syndrome, etc. Organisms transformed with the DNA sequences can be used
CC computer readable medium.

Sequence 5000 BP; 1377 A; 990 C; 641 G; 1808 T;
Search completed: August 7, 2000, 09:21:12 Job time: 445 sec
                                                                                                                                                                                                                                                                                                                                                                                                                Ouery Match 3.4%; Score 32; DB 1; Length 5000; Best Local Similarity 29.2%; Pred. No. 1.9; Matches 21; Conservative 26; Mismatches 25; Indels
                                                                                                                                                              792 uaccuuguguuu 803 : |:::| ::
562 TTTCTTCTGATT 573
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30-JUL-1997.
07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR, Kunsch CA, Rosen CA;
                                                                                                                                                                                                                                                                      502 TGTTTTTGGAGCTTCTCTAAAACTGTAGTAACCAAAGTAATTATTAGTAACTTTATTCGT 561
                                                                                                                                                                                                                                                                                                                          misc_feature
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Sequence 1, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 9, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 10, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 12, Appli Sequence 13, Appli Sequence 14, Appli Sequence 16, Appli Sequence 17, Appli Sequence 17, Appli Sequence 18, Appli Sequence 19, Appli Sequence 11, Appli Sequence 11, Appli

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Post-processing:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
  nucleic search, using sw model
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/5B_COMB.seq: *
/cgn2_6/ptodata/1/ina/5C_COMB.seq: *
/cgn2_6/ptodata/1/ina/5C_COMB.seq: *
/cgn2_6/ptodata/1/ina/6_COMB.seq: *
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US-08-232-463-14
US-08-793-599-1
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US-08-687-080-105
US-09-26-568-18
US-09-211-640-1
US-09-211-640-1
US-09-211-640-1
US-08-08-68-9458-1
US-08-08-22-1778-17
US-08-22-1778-17
US-08-22-1778-17
US-08-22-1778-17
US-08-22-1778-12
US-08-162-081B-34
US-08-162-081B-34
US-08-162-081B-34
US-08-162-081B-32
US-08-724-3948-22
US-08-724-3948-22
US-08-724-3948-22
US-08-689-421-32
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                            sequence
                            14. Appl
13. Appl
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                              ; IMMEDIATE SOURCE: ; CLONE: pTZgpt-
US-08-232-463-14
                                                                                                                                                 CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/07/935,313

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/114 I

REFERENCE/DOCKET NUMBER: 30472/114 I

TELECOMMUNICATION INFORMATION:

TELEFAX: (703)63-4300

TELEFAX: (703)63-4300

TELEFAX: (703)63-4109

TELEFAX: 899149

INFORMATION FOR SEQ ID NO: 14:

SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs

TYPE: DISTINCT OF THE PAIR OF TH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 14, Application Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: VA
COUNTRY: USA
ZIP: 22313-0299
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT
NUMBER OF SEQUENCES: 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 1500 -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS
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                                                                                              STRANDEDNESS: single TOPOLOGY: linear
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>. 5670367
                                                                                                                                        nucleic acid
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1800 Diagonal Road,
                                                    przgpt-F1s
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US-08-676-967-2
US-08-676-974-2
US-08-676-974-2
US-08-97-981-802-1
US-08-911-722-1
US-08-781-722-3
US-08-781-721-15
US-08-937-271-15
US-08-937-271-15
US-08-937-271-15
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Suite

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30472/114 IMMU

Total number

Scoring table: Sequence: Title: Perfect score:

Minimum DB seq Maximum DB seq Minimum

Matches

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Gaps

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us-08-793-599-3/c
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APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: KIHARA, MAROTO
TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
FILE REFERENCE: 2589-0056-0 pcr
CURRENT APPLICATION NUMBER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER APPLICATION NUMBER: DT-05/5
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1995-07-05
EARLIER FILING DATE: 1995-07-05
                                                                                                                                                                                                                                                                                                                                                                                                                    ; SEQ ID NO 1
; LENGTH: 1276
; TYPE: DNA
; ORGANISM: Barley
JS-08-793-599-1
                                                                               Sequence 3, Application US/08793599 Patent No. 5952489
                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local :
                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/08793599 Patent No. 5952489
                APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                   136 ATTAATGTTCAAACGTGTCCACTAGAGTTCAAGTCTCAGACTTGACATTTGTGTTTGCAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1211 אייייין אייייין אייייין איייין איייין אייייין אייייין אייייין אייייין אייייין אייייין אייייין אייייין איייי
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| 76 GTTTCCTTAATTTATTTCATGCCTT 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        703 gcccugaucugagcucugugguaucugauuguuguuggaccgucuccaagacggugauaa 762
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13; Conservative 156;
       OKADA, YUKIO
YOSHIGI, NAOHIRO
ITO, KAZUTOSHI
                                                                                                                                                                                                                                                                                           3.3%; pred. No. ...
27.1%; pred. No. ...
-+ive 28; Mismatches
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4.5%; Pred. No. 0.016;
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CURRENT APPLICATION NUMBER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1995-07-05
EARLIER FILING DATE: 1995-07-05
NUMBER: OF SEQ ID NOS: 3
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 2142
TYPE: DNA
ORGANISM: Barley
US-08-793-599-3
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US-08-687-080-105/c
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                                                                                                                   TELEPHONE: (415) 324-081
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
MOLECULE TYPE: HYPOTHETICAL:
                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 13158 base pai
                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 46
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NERAL INFORMATION:
APPLICANT: Gregory
TITLE OF INVENTION:
                               STRANDEDNESS:
TOPOLOGY: lir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U. ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 350 Camu
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23;
                                            i: 13158 base pairs nucleic acid DEDNESS: double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gregory Dolganov
                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version
                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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            DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Floppy disk
                                                                                                                                                    324-0880
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27.1%;
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Pred. No. 1.9;
28; Mismatches
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RESULT

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Matches

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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-687-080-105
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; OTHER INFORMATION: sequence
US-09-226-568-18
                                                                                                                                                                                                                                                                                                     US-08-077-848A-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US-09-226-568-18/c
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Best Local Similarity 34.v
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 18
LENGTH: 3934
                                                                                                                                                                                                                                     Sequence 1, Application US/08077848A Patent No. 5470955
GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dean, Nicholas M.
APPLICANT: Marcusson, Eric G.
TITLE OF INVENTION: Antisense Modulation of No.
TITLE OF INVENTION: bcl-2-Related Proteins
FILE REFERENCE: ISPH-0337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                       TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
                                                                                                         ADDRESSEE: Spensley Horn Jubas & STREET: 1880 Century Park East, S CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity 56.2
27; Conservative
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                                                                                                USA
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Pred. No. 11;
9; Mismatches
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Pred. No.
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   Version #1.25
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20;
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; LOCATION: 61..1110
; OTHER INFORMATION:
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Best Local
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pair:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-7
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
TELEFAX: (619) 455-5110
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TOPOLOGY: linear
MOLECULE TYPE: DNA
IMMEDIATE SOURCE:
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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                                                                                                                                                   PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
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TOCATION: 61..1110
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                                                                                                                                                                                                                                                                                                                                                CITY: Los Angeles
STATE: California
                                                                                                                   FILING DATE:
                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                   FILING DATE:
                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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l Similarity 56.2%;
27; Conservative
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1880 Century Park East, Suite 500
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619) 455-5110
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amino acid 227 = A; when nucleotide
acid 227 = V."
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Pred. No. 11;
9; Mismatches
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                                                      PD-2845
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Query Match Best Local :

3.1%; 56.2%;

Score 28.8; Pred. No. 11

DB 6;

Length 3946;

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PCT-US94-03547-1/c
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GENERAL INFORMATION:
APPLICANT: The Johns Hopkins Univ
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Best Local Similarity
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TELEFAX: (619) 455-5110
NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                         NAME: Wetherell, Jr., Ph.D., John W. REGISTRATION NUMBER: 31,678
REFERENCE/DOCKET NUMBER: FD-2845
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
NAME/KEY: CDS
LCCATION: 61..1110
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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MEDIUM TYPE: Floppy disk
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LENGTH: 3946 base pairs
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                                                                                                                                                                                                TYPE: nucleic acid
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LOCATION: 61..1110
OTHER INFORMATION:
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1880 Century Park East, Suite 500
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                                                                                                                                               DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: PCT/US94/03547
31-MAR-1994
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       /note= "When nucleotide 740 = C, amino acid 227 = A; when nucleotide 740 = acid 227 = V."
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Pred. No. 11;
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RESULT 9
US-08-068-945A-1
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                                                                                                                                                                                                                                                                                APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION UNMER: SE 9300902-5
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-05
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                    MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: SE 9201809-2 FILING DATE: 11-JUN-1992 PRIOR APPLICATION DATA:
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                                                 TISSUE TYPE: Mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: SE 9201826-6 FILING DATE: 12-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/068,945A FILING DATE: 27-MAY-1993
 LOCATION:
                                                                                                                       TOPOLOGY:
                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: New York
                                                                       ORGANISM:
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27; Conserv
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Lidberg, Ulf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Carlsson, Peter
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                                                                                                                         linear
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join(1653..1727, 4071..4221, 4307..4429, 4707
                                                                                                                                                                                                                                                   (212)819-8783
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                                                                                                       DNA (genomic)
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US-08-068-945A-1
US-08-442-806-1
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Best Local Similarity
Matches 51; Conserv
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LOCATION:
FEATURE:
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LOCATION:
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NAME/KEY:
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                                                                                                 GGAGTTTCATCGTGTTAGCTAGGATGATCTCG 7258
                                                                                                                                                                                                   CTGGGACTACAGGCACATGCCATGCCCAGATAATTTTTCTGTGTGTTTAGTAGGGAT 7226
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join(1722..1727, 4071..4221, 4307..4429, 4707
...4904, 6193..6323, 6501..6608, 6751..6868, 8335
...8521, 8719..8922, 10124..10321, 10650..11391)
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10124..10321
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8719..8922, 10124..10321, 10650..11394)
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33.6%; Pred. No. 21;
tive 24; Mismatches
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Sequence 1, Patent No.
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TELEFAX: (212)54-8113
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pai
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 3:
FILING DATE: 03-JUL-1:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: SE 9201809-2
FILING DATE: 11-JUN-1992
PRIOR APPLICATION NUMBER: SE 9201826-6
APPLICATION NUMBER: SE 9201826-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 00
FILING DATE: 27-MAY-1993
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: SE 9.
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J
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                                                                                       FEATURE:
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ZIP: 100
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LOCATION:
LOCATION:
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STATE: New York
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                                                                                                                                                                                          TISSUE TYPE:
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10036-2787
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Lidberg, Ulf
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..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
mat_peptide

join(1722..1727, 4071..4221, 4307..4429, 4707)

.4904, 6193..6323, 6501..6608, 6751..6868, 833

.8521, 8719..8922, 10124..10321, 10650..11391)

RMATION: /EC_number= 3.1.1.1
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03-JUL-1992
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Encoding Human BSSL/CEL
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RESULT 11
US-08-222-177A-17
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                                                       Sequence 17, Application US/08222177A Patent No. 5582979 GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                        Query Match
          APPLICANT: Weber, James L.

TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                 7167
                                                                                                                                           NAME/KEY:
LOCATION:
FEATURE:
CORRESPONDENCE
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4071..4221
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                                                                                                                                                                                                                                                                                                          Score 28.8;
Pred. No. 21;
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APPLICATION NUMBER: US 07/341
APPLICATION UMBER: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION UNMBER: 30,492
REFERENCE/DOCKET NUMBER: 0986
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION 1831-2100
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                                                                                                  IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "Only or PUBLICATION INFORMATION:
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CHROMOSOME/SEGMENT:
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MEDIUM TYPE: Floppy disk
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OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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PRIOR APPLICATION DATA:
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AUTHORS: Weber, J. L.
AUTHORS: May, P. E.
TITLE: Dinucleotide repeat polymorphism at the
TITLE: D3S240 locus
JOURNAL: Nucleic Acids Res.
                                                                                                                                                                               NAME/KEY:
LOCATION:
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IDENTIFICATION METHOD: experimer
OTHER INFORMATION: /evidence- ps
OTHER INFORMATION: /standard_nam
OTHER INFORMATION: /citation= ([
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STREET: 8000 E
CITY: Madison
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LOCATION:
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LOCATION:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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1..221
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/evidence= EXPERIMENTAL
/standard_name= "PCR pri
/citation= ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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US-08-222-177A-52
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Best Local Similarity
Matches 28; Conserv
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GENERAL INFORMATION:
APPLICANT: Weber, James L.
                                                                                                                                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY_AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                              INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 278 base pairs
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AUTHORS: Weber, James
AUTHORS: May, Paula E
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING
NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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MOLECULE TYPE:
ORIGINAL SOURCE:
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DATE: 1989
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                                              TYPE: nucleic acid
STRANDEDNESS: double
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                                  TOPOLOGY:
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Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
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8000 Excelsior Drive, Suite 401
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                DNA (genomic)
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Pred. No. 3.3;
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; VOLUME: 44
; PAGES: 388-:
; DATE: 1989
US-08-222-177A-52
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Best Local
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NAME/KEY: repeat_region
76..118
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IDENTIFICATION METHOD: (
OTHER INFORMATION: /sta
OTHER INFORMATION: /cit
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IDENTIFICATION METHOD: experime:
OTHER INFORMATION: /evidence-E:
OTHER INFORMATION: /standard_nar
OTHER INFORMATION: /citation-()
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OTHER INFORMATION:
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AUTHORS:
                     765 uaagucgugguuuguguguuuguuaccuuguguuuguucgu 809
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OTHER INFORMATION: /ev
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JOURNAL:
                                                                                                                                                                                                                                                                                                           AUTHORS:
                                                          4 CCATTTCTGGGCGCACATGTATCTAGCCATGGTAGCACAGGCCGGGAAGCTCTGTGCTGG 63
                                                                                                                th 3.0%;
l Similarity 30.5%;
32; Conservative 25
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S: Wasmuth, J. J.
Mapping of human chromosome 5 microsatellite polymorphisms
                                                                                                                                                                                                                                                                                                                                                       1991
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Abundant Class of Human DNA Polymorphisms Which Can Be Typed Using the Polymerase C
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Kwitek, A. E.
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/evidence= EXPERIMENTAL
/standard_name= "PCR primer"
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/rpt_family= "(dC-d
/citation= ([2])
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/evidence= EXPERIMENTAL
/standard_name= "PCR pr
/citation= ([1])
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                                                                                                                    25;
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Pred. No. 3.8;
                                                                                                                      Mismatches
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                                                                                                                                              DB 1; Length 278;
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                                                                                                                                                                                                                                                                                  Chain
                                                                                                                      Indels
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RESULT 13 US-08-323-170B-1/c

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US-08-162-081B-34
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; LOCATION:
US-08-323-170B-1
                                                                                                                                      Sequence 34, Application US/08162081B Patent No. 5824492
                                                                                                                                     Patent No.
                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
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                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (415) 576-030
APPLICANT: Joseph; Otsu, Masayuki; ranayuku, wenge, APPLICANT: Stefano; Gout, Ivan Tarasovitch TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, TITLE OF INVENTION: THEIR PREPARATION AND USE
                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                    4797 GGTCCTAATGGTGATTTGACATTATATTTTTTTTTTTTAAATCAACACATATACATTTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 9636 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-JAN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Quine, Jonathan A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010,409
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MEDIUM TYPE: Floppy disk
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ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
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FILING DATE: 13-OCT-1994
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                                                           Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu
Bala; Waterfield, Michael Derek; Parker, Peter
Joseph; Otsu, Massyuki; Panayotou, George; Volini
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Kaslow, David C.
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576-0300
7 NO: 1:
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Pred. No. 31;
23; Mismatches
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Sequence 34, Approx
Sequence 34, Approx
No. 5846824
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                                                                                            COUNTRY: U
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APPLICATION NUMBER: US/08/162/0
FILING DATE: February 7, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/00
FILING DATE: 13 APTI1 1993
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALITY INFORMATION:
REGISTRATION NUMBER: 1494
REFERENCE/DOCKET NUMBER: LUD 52
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (212) 838-38 INFORMATION FOR SEQ ID NO:
               COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DO
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                   APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia, APPLICANT: Stefano; Gout, Ivan Tarasovitch
                                                                                                                                                                                                                                                                     TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2535 GGGACTTATTGAGGTG 2550
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LENGTH: 3240 base pair
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York
STATE: New York
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OPERATING SYSTEM:
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                                                                                                                                                               New York
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                                                                                                                                                                                           805 Third Avenue
                                                                                                                                                                                                                                                      Stefano; Gout, Ivan Tarasovitch
VENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
VENTION: THEIR PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3240 base pairs
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                                                                                    Diskette, 5.25 inch, 360 kb storage
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February 7, 1994
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Pred. No.
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CLASSIFICATION: 435

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/163.081

FILING DATE: FEBRUARY 7, 1994

APPLICATION NUMBER: 08/163.081

FILING DATE: FEBRUARY 7, 1994

APPLICATION NUMBER: 08/163.081

FILING DATE: 13 APPLICATION NUMBER: 12/1993/00761

FILING DATE: 13 APPLICATION NUMBER: 12/1993/00761

FILING DATE: 13 APPLICATION NUMBER: 12/1993/00761

APPLICATION NUMBER: 12/1993/00761

FILEPONE: (212) 686-9200

TELEPHONE: (212) 686-9200

TELEPAX: (212) 686-9200

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gb_est25: gb_est26: gb_est27: gb_est28: gb_est29: gb_est30: gb_est31: gb_est31:

em_est21:* em_est22:*

em_est23:* em_est24:* em_est20:*

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Maximum DB seq length: 1000000
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gb_gss18:*
gb_gss19:*
em_gss13:*

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CNS00LT2 1101 bp DNA GSS 14-JUN-1999
Drosophila melanogaster genome survey sequence TET3 end of BAC:
BACR48P19 of RPCI-98 library from Drosophila melanogaster (fruit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              is the number of results predicted by chance to have a tter than or equal to the score of the result being printed, ived by analysis of the total score distribution.
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AL105745 Drosophil
AL098710 Drosophil
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AL098851 Drosophil
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AL056652 Drosophil
AL071370 Drosophil
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AUTHORS
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VERSION
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                      anaagucgugguuuguguuuguuuguuaccuuguguuuguucgucacuugu
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                                                                                                     KDKTKKKKKAATTTTKKKKGKKKKKAAKKKKAADRTKKTKWDAAAAAAKKTKDKGK
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45; Conserv
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR48P19"
/note="end : TET3"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BACR14N21 of RPCI-98 library from
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Similarity 5.8%; Pred. No. 0.029;
14; Conservative 129; Mismatches
                   fruit fly.
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38 c 17
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN05C05"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP brosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo. NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic Strain y2; on bw sp, the same strain used for the BDGP's Pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be found at http://Dacpac.med.buffalo.edu/drosophila_bac.htm.
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Submitted (02-JUN-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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187; Mismatches
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1225)
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN15C20"
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segref@genoscope.cns.fr
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/clone="BACN17J04"
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/plasmid="pBeloBAC11"
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila...
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               fly), genomic
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                                  CNS016TE 1010 UP
Drosophila melanogaster genome
BACN16C05 of DrosBAC library fr
flv), genomic survey sequence.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="DrosbAC"
/clone="BACN15017"
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BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genovieve Payan. It has been constructed in the vector
fruit fly.
fruit fly.
Drosophila melanogaster
Drusophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
Etherygota; Neoptera; Endopterygota; Diptera; Brachyco
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
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Drosophila melanogaster
BACN03M12 of DrosBAC lik
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) of this Project (EDGP) of this Prosophila melanogaster BAC hattp://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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/plasmid="pBeloBACI1"
/db_xref="taxon:7227"
/clone_lib="DrosBAC"
/clone="BACN16K15"
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                                  BP 191 91006 EVRY cedex -
                                                                                                                                                                                                                                                                                                                                                                            CNS006QP 902 bp DNA Drosophila melanogaster genome BACR14J09 of RPCI-98 library fr
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Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
                                                                      Submitted (02-JUN-1999) Genoscope -
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30; Conservative
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                                                                                                                                         scomorpha; Ephydroidea; Drosophilidae; Drosophila (bases 1 to 902)
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nation of this BAC-end
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/clone="BACN03M12"
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/plasmid="pBeloBAC11"
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12.2%; Pred. No. 0.69
tive 107; Mismatches
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(E-mail : seqref@genoscope.cns.f)
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Pterygota; Meotera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 937)
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org.rbg.plcoophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department of
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fi
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Drosophila melanogaster genome survey sequence T7 end of BAC #
BACR14J21 of RPCI-98 library from Drosophila melanogaster (fruit
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP).
The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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23; Mismatches 143;
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- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of Determination with the Berkeley Drosophila Genome Project (BDGP)

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Manmoser in Pieter de Jong's laboratory in the Department
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
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                   Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part collaboration with the European Drosophila Genome Project (EDG http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Centre Library (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain Billaud at CEPH (Dros BAC) was made by Alain B
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Similarity 10.3%; Pr
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/db_xref="taxon:7227"
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Drosophila melanogaster

Drosophila; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Eukaryota; Meoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1201)
 Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segrefégenoscope.cns.fr - Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC 11brary (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC
                                                                                                                                                                                                                                                                                                           CNS016FD 1201 bp DNA GSS 26-JUL-1999
Drosophila melanogaster genome survey sequence T7 end of BAC
BACN15E24 of DrosBAC library from Drosophila melanogaster (fri
fly), genomic survey sequence.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_11b="DrosBAC"
/clone="BACN16J16"
/note="end: T7"
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_11b="DrosBAC"
/clone="BACN15E24"
/note="macnd: T7"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk -. This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

[ bases 1 to 1159)
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/clone="BACN17J04"
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/plasmid="pBeloBAC11"
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Pterygota; Neoptera; Endopterygota; Diptera; Brachyce
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns
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Pterygota; Neoptera; Endopterygo
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/organism="Drosophila m/
/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib="prosBAC"
/clone="BACN15C20"
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tive 165; Mismatches
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Endopterygota; Diptera; Brachycera;
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                   fruit fly,
Drosophila melanogaster
Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                      CNS016VI 995 bp DNA GSS
Drosophila melanogaster genome survey sequence
BACN16K15 of DrosBAC library from Drosophila me
fly), genomic survey sequence.
AL107256
Genoscope.
Direct Submission
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Neb: www.genoscope.cns.fr)

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191 c 154
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
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/clone="BACN16C05"
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Drosophila melanogaster genome survey sequence SP6 end of BAC
BACNO3M12 of DrosBAC library from Drosophila melanogaster (fruit
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                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
                                                                                                   fruit fly.
Drosophila melanogaster
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AL098287.1 GI:5609898
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/clone="BACN16K15"
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/plasmid="pBeloBAC11"
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- Web : www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Droscophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - Jhis Droscophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre 1:Droary Coros BAC) was made by with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector pBeloBAC11.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster genome survey sequence TET3 end of BAC # BACR14J09 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
Web: www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as par collaboration with the Berkeley Drosophila Genome Project (BDC The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila
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AL065804
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/plasmid="pBeloBAC11"
/db_xref="taxon:7227"
/clone_lib-"DrosBAC"
/clone="BACN03ML2"
/note="end : SPE"
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L Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage:
BP 191 91006 EVRY cedex - FRANCE (E-mail: segref@genoscope.cns.fr

- Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information melanogaster genome using these BACs. For further information melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecor digestion of Drosophila DNA provided by the BDGP from the lisogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/note="end: TET3"
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Determination of this BAC-end sequence was carried out as part of collaboration with the Berkeley Drosophila Genome Project (BDGP) The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila neclanogaster BAC ilbrary was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pieter de Jong's laboratory in the Department Cancer Genetics at the Roswell Park Cancer Institute in Buffalo NY. The library is named RPCI-98 and was constructed by partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTYKYGTGCTCTCTSKTKKYTSSTKCKCCGSGCCCTCSYGYYGYCYGCSYSTBYGSSYCC
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                                                                                                                                                                                                                                   Genoscope.
Direct Sub
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 910)
                                                                                                                                                                         Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster genome survey sequence T7 end of BAC # BACR14721 of RPCI-98 library from Drosophila melanogaster (fruit fly), genomic survey sequence.
AL065629
AL065629.1 GI:4944698
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14B21"
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Submitted (02-UN-1999) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a Determination with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster BAC library was prepared by Kazutoyo Osoegawa and melanogaster the Pieter de Jong's laboratory in the Department of Aaron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial Ecorl digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's
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Dukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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/db_xref="taxon:7227"
/clone="ib="%PCI-98"
/clone="hcR14J21"
/clone="end: T7"
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Direct Submission
Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
Submitted (23-JUL-1999) Genoscope - FRANCE (E-mail : seqref@genoscope.cns.fr
BP 191 91006 ENYCope.cns.fr)
FOR STANCE (E-mail : seqref@genoscope.cns.fr

Www.genoscope.cns.fr)
Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - Collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain
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AL106675.1 GI:5623167
                                             Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins.
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1201)
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/clone=_1lb="DrosBAC"
/clone="BACN16J16"
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7.5%; Pred. No. 1.9;
tive 108; Mismatches
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                            unuguuuguuaccuuguguuuguuc
                                                          TTTTTTTTTTYGGGTYAABTTTTKTGCGYYKCSGTTTTTTKGGTTSTKTKKKGGCYY 1045
                                                                                                                  SCCCTTTTTSGGGCTKGTTBTKGBGYCCSSSSGSSKYSCSCTCYYYTTTTTTTCTT
                                                                                                                                       ggacgcugccgggaagcuccaccuccgcucagcaggggacgcccugaucugagcucugug
                                                                                                                                                                             YTYTWTTTKCSGGKTCYBCGGKTYTTBCCYTTTBKBBBGYGGGSRCGTSGGGYTTYYGSC
                                                                                                                                                                                                      gccgguaaguaaguacuugauuuugguaccucgcgaggguuugggaggaucggaguggcg
                                                                                                                                                                                                                                         GGGCCCCCYCTTCTCGGYTTYYBBBITKKYYYTTAYKTGCCTABKTTTBKTTTYTTBTKTK 865
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45; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 149;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1. .1201
/organism="Drosophila melanogaster"
/plasmid="pBeloBaCI1"
/db_xref="taxon:7227"
/clone_lib="DrosBaC"
/clone="BACN15E24"
/note="end : T7"
/note="end : T35 g 325 t 243 ot
                                                                                                                                                                                                                                                                                                                                                                                                                                    6.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 36.4; DI
Pred. No. 2.6;
49; Mismatches
                            445
1070
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Search completed: August 7, 2000, 11:56:08 Job time: 9742 sec

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; CLONE: pTZgpt-F1s
US-08-232-463-14
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                                                                                                                                                                                                   APPLICATION NUMBER: EP 91 114 300.6 FILING DATE: 26-AUG-1991 ATTORNEY/AGENT INFORMATION: NAME: BENT, Stephen A. REGISTRATION NUMBER: 29,768 REFERENCE/DOCKET NUMBER: 30472/114 IMM TELECOMMUNICATION INFORMATION: TELEPHONE: (703)836-9300 TELEPAX: 800145 (83-4109 TELEFAX: 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 14, Application US/08232463
Patent No. 5670367
GENERAL INFORMATION:
                                                                                                                         TELEX: 899149
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pair
                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UI
FILING DATE:
APPLICATION NUMBER: UI
ETITUS DATE:
APPLICATION NUMBER: UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLDOX VIRUS
NUMBER OF SEQUENCES: 52
                                       IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Foley & I
                                                           STRANDEDNESS:
TOPOLOGY: lin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: Alexandria
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                                                                                       nucleic acid
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1800 Diagonal Road, Suite 500
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US-09-166-186-107
US-09-166-1898-1
PCT-US93-01720-1
US-08-254-404-19
US-08-254-404-19
US-08-254-404-19
US-08-37-7451E-19
US-08-37-771-12
US-08-37-771-12
US-08-37-771-11
US-08-38-7271-16
US-08-937-771-11
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US-09-225-170-11
US-08-781-802-9
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Sequence 9, Applil
Sequence 10, Applil
Sequence 10, Applil
Sequence 1 Applil
Sequence 1, Applil
Sequence 1, Applil
Sequence 2, Applil
Sequence 3, Applil
Sequence 19, Applil
Sequence 19, Applil
Sequence 16, Applil
Sequence 16, Applil
Sequence 17, Applil
Sequence 17, Applil
Sequence 18, Applil
Sequence 18, Applil
Sequence 19, Applil
Sequence 11, Applil
Sequence 2, Applil
Sequence 2, Applil
Sequence 19, Applil
Sequence 19, Applil
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Minimum

Total number of hits satisfying chosen parameters:

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243080 seqs, 68777915 residues

IDENTITY_NUC
Gapop 10.0 , Gapext 1.

Scoring table:

Title: Perfect score:

US-09-214-124-2 578

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Sequence:

OM nucleic -

nucleic search, using

sw model

GenCore version Copyright (c) 1993 - 2000

4.5 Compugen Ltd

August 7, 2000, 09:28:16; Search time 172.61 Seconds (without alignments) 460.618 Million cell updates/sec

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Maximum

DB seq

length: 0 length: 1000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

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943 2055 2277 2277 2277 2643			the number of retthan or equal to d by analysis of
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			of interest of int
US-08-705-875A-1 US-07-842-349-1 US-08-676-967-2 US-08-676-974-2 US-08-676-974-2 US-08-781-802-11	US-08-162-081B-34 US-08-780-872-34 US-08-162-081B-32 US-08-780-872-32 US-08-689-421-32 US-08-843-530B-1 US-09-010-398-14		sults prediction the score the total summaries
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APPLICANT: CARDA, YUKIO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: TOS, KAZUTOSHI
APPLICANT: KHARA, MAKOTO
TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
FILE REFERENCE: 2589-0056-0 PCT
CURRENT APPLICATION UNUMER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
UNUMER OF SEQ ID NOS: 3
SOTTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 1276
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                                              Sequence 3, Application US/08793599 Patent No. 5952489 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                               Query Match 5.3%;
Best Local Similarity 27.1%;
Matches 23; Conservative 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08793599 Patent No. 5952489
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
APPLICANT: OKADA, YUKIO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: ITO, KAZUTOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1031 TICCGAGCTIGGCIGCAGGICGAGGGAGCTIGCGATYYYYYYYYYYYYYYYYYYYYYYYYYY 1090
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                                                                                                                                                                                  428 guuaccuuguguuuguucgucacuu 452 | :: | | :: :: :: :: | ::
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                                                                                                                                                                                                                                                                                                   28; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 37.6; DB
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                 Score 30.6; D. Pred. No. 1.1;
                                                                                                                                                                                                                                                                                                                                DB 4; Length 1276;
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RESULT 4
US-08-687-080-105/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: KIHARA, MAKOTO
TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
FILE REFERENCE: 2589-0056-0 PCT
CURRENT APPLICATION NUMBER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1996-07-05
EARLIER FILING DATE: 1995-07-05
EARLIER FILING DATE: 1995-07-05
EARLIER FILING DATE: 1995-07-05
NUMBER OF SEQ ID NOS: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2142
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Best Local Similarity
                                                                                                                                                                                                  CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/687,080
FILING DATE: 17-JUL-1996

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/592,126
FILING DATE: 26-JAN-1996
ATTORNEY/ACENT INFORMATION:
NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REGISTRATION NUMBER: 4600-0111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Gregory Dolganov
                                                                                       TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 13158 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Human RAD50 Gene and NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dehlinger & Associates
STREET: 350 Cambridge Avenue, Suite 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy
                                                                                                                                                                  TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 324-0880
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            136 ATTAATGTTCAAACGTGTCCACTAGAGTTCAAGTCTCAGACTTGACATTTGTGTTTGCAA 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS_MS-DOS
SOFTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 350 Cana
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 94306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                               TOPOLOGY: linear
                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GTTTCCTTAATTTATTTCATGCCTT 52
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                                                                     nucleic acid
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DNA (genomic)
                                                       double
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                                                                                                                                105:
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Pred. No. 1
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; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; INDIVIDUAL ISOLATE:
; INDIVIDUAL ISOLATE:
US-08-687-080-105
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US-08-077-848A-1/c
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Best Local Similarity
Watches 27; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: Description of Artificial Sequence: antisense; OTHER INFORMATION: sequence US-09-226-568-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         В
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Best Local Similarity 34.0%;
Matches 18; Conservative
                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/08077848A Patent No. 5470955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dean, Nicholas M.
APPLICANT: MATCUSSON, Eric G.
TITLE OF INVENTION: Antisense Modulation of No.
TITLE OF INVENTION: bcl-2-related Proteins
FILE REFERENCE: ISPH-0337
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/226,568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Ackermann, Elizabeth J.
APPLICANT: Bennett, C. Frank
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10896 TITTITCTCTTATAGCCTAATCTTGGAAGTGAAGGGAATTCTTATTCCTGCTG 10844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3934
TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
                                                                                                                      STREET: LOS Angeles
CITY: LOS Angeles
STATE: California
                                                                                                                                                                                                                                         APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIB
TITLE OF INVENTION: POLYP
                                                                                     COMPUTER READABLE FORM:
                                                                                                                                                                                                           NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                             600 CTCCAGCGACTGCCGGTACAACTCGTCCTCCTCCTCCTGCTGGCGG
       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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                                                                                                       ZIP: 90067
                                                                                                                                                                                          ADDRESSEE:
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APPLICATION DATA:
                                                                                                                                                                    1880 Century Park East,
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                                                                                                                                                                        Spensley Horn Jubas & Lubitz
80 Century Park East, Suite 500
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56.2%;
                                                                                                                                                                                                                                              POLYPEPTIDE
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Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 28.8; D
Pred. No. 8.1;
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OTHER INFORMATION: ACTUS-08-077-8488-1
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (619) 455-510
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Haile, ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION: APPLICANT: Craig,
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                ATTORNEY/AGENT INFORMATION:
NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
                                                                                                                                                                                    CURRENT APPLICATION DATA: APPLICATION NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
 TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                  PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
mes 27; Conserv
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CLASSIFICATION: 424
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                                  REFERENCE/DOCKET NUMBER:
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TELEPHONE:
                                                                                                      FILING DATE
                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                      FILING DATE
                                                                                                                                                                                                                                                                                                                      COUNTRY:
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                                                                                                                    08/441,375
                                                                                                                                                                                    US/09/211,640
                                                38,347
                                    PD-2845
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Pred. No. 8.1;
9; Mismatches
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Length 3946;

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PCT-US94-03547-1/c
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                                                                                                                                                                                   TELEPHONE: (619) 455-5100
TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 3946 base pairs
TYPE: nucleic acid
GTEANDENESC: 6:010
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                       TOPOLOGY: 1
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
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LENGTH: 3946 base pairs
TYPE: nucleic acid
                                                                                                                       IMMEDIATE SOURCE:
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LOCATION: 61..1110
OTHER INFORMATION: 0
OTHER INFORMATION: 6
OTHER INFORMATION: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
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                                 LOCATION: 61..1110 OTHER INFORMATION:
   OTHER INFORMATION: OTHER INFORMATION:
                                                                                                       CLONE:
                                                                                                                                                                       STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                              NAME: Wetherell, Jr., Ph.D. REGISTRATION NUMBER: 31,678 REFERENCE/DOCKET NUMBER: FD.
                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: FILING DATE: 31-MAI CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
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                                                                     NAME/KEY:
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: California
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                                                                                                        mcl-1
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1880 Century Park East, Suite 500
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                                                                                                                                                       linear
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                                                                                                                                       DNA (genomic)
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56.2%;
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amino acid 227 = A; when nucleotide 740 = T,
acid 227 = V."
/note- "When nucleotide 740 = C, amino acid 227 = A; when nucleotide 740 = T, amino acid 227 = V."
                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US94/03547
                                                                                                                                                                                                                                                                                                                                                Ph.D., John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 28.8; DE Pred. No. 8.1; 9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 5; Length 3946;
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RESULT 9
US-08-068-945A-1
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Best Local :
                                                                                                                                                                                                           TELEFAX: (212)354-8113
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993
                                                                                                                                                                                                                                       REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212,819-8783
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9:
FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
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OPERATING SYSTEM: PC-DO
SOFTWARE: Patentin Rela
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                               FILING DATE: 19-MAR-1993 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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                                                                                    MOLECULE TYPE: TO SRIGINAL SOURCE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/068,945A FILING DATE: 27-MAY-1993 CLASSIFICATION: 435
                                                                                                                                     LENGTH: 11531 base pairs TYPE: nucleic acid STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: SE 9201826-6 FILING DATE: 12-JUN-1992
                                                  ORGANISM: HOTISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: United States ZIP: 10036-2787
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LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: New York
                                                                                                                        TOPOLOGY:
                                                                                                                                                                     ENGTH:
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27; Conserv
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Tornell, Jan
                                            Homo sapiens
E: Mammary gland
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Enerback, Sven
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
join(1653..1727, 4071..4221, 4307..4429, 4707
                                                                                                                      linear
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idberg, Ulf
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                                                                                                    "DNA (genomic)
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56.2%;
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Pred. No. 8
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RESULT 10
US-08-442-806-1
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; LOCATION:
US-08-068-945A-1
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Best Local S
Matches 51
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LOCATION:
FEATURE:
                                                 7227 GGAGTTTCATCGTGTTAGCTAGGATGATCTCG
                                                                                                                                                      7107 GCTCACTGCAACCTCCACCTCGGGTTCAAGTGATTCTCTGACTCAACCTCCCATGTAG 7166
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NAME/KEY:
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                                                                  425 uuuguuaccuuguguuuguucgucacuugucg 456
                                                                                                                 365 cugauuguuguuggaccgucuccaagacggugauaauauaagucgugguuuguguuug 424
                                                                                                                                                                     305 gcugccgggaagcuccaccuccgcucagcaggggacgcccugaucugagcucugugguau 364
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51; Conservative
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6193..6323
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8335.
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join(1722:.1727, 4071..4221, 4307..4429, 4707

..4904, 6193..6323, 6501..6608, 6751..6868, 8335

...8521, 8719..8922, 10124..10321, 10650..11391)
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11491..11531
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10650..11490
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10124..10321
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6751..6868
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4307..4429
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1611..1617
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..8521, 8719..8922, 10124..10321, 10650..11394)
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6501..6608
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4071..4221
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1641..1727
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33.6%; Pred. No. 14;
vative 24; Mismatches
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                                                   7258
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Sequence 1,
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PRIOR APPLICATION NUMBER: SE 920:

APPLICATION NUMBER: 12 JUN-1992
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 11531 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Sterner, Richard J.
REGISTRATION NUMBER: 35,372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                             MOLECULE TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION UDATA:
APPLICATION WHERE: US 08/068,945
FILING DATE: 27-MAY-1993
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                                                                                                                                                   FEATURE
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                                                                                   LOCATION:
LOCATION:
LOCATION:
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                                                     NAME/KEY:
                                                                                                                                 NAME/KEY:
                                                                                                                                                                 ORGANISM: HOTISSUE TYPE:
                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: SE 9300902-5 FILING DATE: 19-MAR-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10036-2787
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                                       LOCATION:
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New York
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United States
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Carlsson, Peter
Enerback, Sven
                                                                                 join(1653..1727, 4071..4221, 4307..4429, 4707
..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11394)
mat_peptide

join(1722..1727, 4071..4221, 4307..4429, 4707

.4904, 6193..6323, 6501..6608, 6751..6868, 8335

.8521, 8719..8922, 10124..10321, 10650..11391)
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E: Mammary gland
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Encoding Hum
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US-08-222-177A-17
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US-08-442-806-1
                                                                                                                                                                                                                                                                                         Query Match
Best Local S
Matches 51
                                                                 Sequence 17, Application US/08222177A Patent No. 5582979
                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                           7107
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
                                                                                                                                         7227 GGAGTTTCATCGTGTTAGCTAGGATGATCTCG 7258
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                                                                                                                                                                                                                                                                                                       Similarity
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8719.
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10650..11490
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10124..10321
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6751..6868
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6193..6323
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4307..4429
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4071..4221
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1641..1727
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33.6%;
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Pred. No. 14;
24; Mismatches
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                                                                                                                                                                                                                                                                                                                   Length 11531;
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLONE: Mfd30
POSITION IN GENOME:
CHROMOSOME/SEGMENT:
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LENGTH: 221 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEPAX: (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Homo sapiens INDIVIDUAL ISOLATE: Cau TISSUE TYPE: Blood IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
                                                                                                                                                                                                                                                                                                                          FEATURE:
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ORIGINAL SOURCE:
                                                                                     PUBLICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                LOCATION: 103..139
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
                                                  AUTHORS:
                                                                                                      IDENTIFICATION METHOD:
OTHER INFORMATION: /ev:
OTHER INFORMATION: /str
                                                                                                                                                                                                             OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                       IDENTIFICATION METHOD: experimental OTHER INFORMATION: /evidence= EXPERIMENTAL OTHER INFORMATION: /standard_name= "PCR primer" OTHER INFORMATION: /citation= ([1])
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                                                                                                                                                                                                                                                 LOCATION: complement (144..163)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
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STREET: 8
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                                                                                                                                                                             NAME/KEY:
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Wisconsin
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                                                                                                                                                           misc_feature
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                               /standard_name= "PCR primer"
/citation= ([1])
                                                                                                      /evidence= EXPERIMENTAL /standard_name= "Only or
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RESULT 12
US-08-222-177A-52
; Sequence 52, Application US/08222177A
; Patent No. 5582979
; Patent No. 5582979
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                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Saca, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                               INFORMATION FOR SEQ ID NO:
                                                                                             SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITLE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
MOLECULE TYPE:
ORIGINAL SOURCE:
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AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      115 TGTGTGTGTGTGTGTGTGTAAAATGTAGAGA 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 uguuuguuaccuuguguuuguucgucacuugucgaca 459
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                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Polence "."
                             TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
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                                                                                                                                                TELEFAX:
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                                                                              LENGTH:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PAGES: 388-396
DATE: 1989
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28; Conservative
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: May, Paula E.
: May, Paula E.
Abundant Class of Human DNA Polymorphisms
Which Can Be Typed Using the Polymerase Chain
                                                                          278 base pairs
                                                                                                                                                (608) 831-2106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: DeWitt Ross & Stevens, S.C. 8000 Excelsior Drive, Suite 401
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             DNA (genomic)
                                              double
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Pred. No. 2.7;
26; Mismatches
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; VOLUME: 44
; PAGES: 388-:
; PATE: 1989
; DATE: 1989
US-08-222-177A-52
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                                                                                                                        Matches
                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                              AUTHORS: Xiao, n. J. D. AUTHORS: McPherson, J. D. AUTHORS: Wasmuth, J. J. TITLE: Mapping of human chromosome 5 microsatellite TITLE: polymorphisms
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OTHER INFORMATION: /rpt_t
OTHER INFORMATION: /rpt_t
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                343 ccugaucugagcucugugguaucugauuguuggaccgucuccaagacggugauaaua 402
                                                                                                                                                                                                                                                                                            TITLE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: complement (198..217)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence- EXPERIMENTAL
OTHER INFORMATION: /standard_name- "PCR primer"
OTHER INFORMATION: /citation- ([1])
 64
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OTHER INFORMATION: /st
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OTHER INFORMATION: /ev
OTHER INFORMATION: /st
OTHER INFORMATION: /ci
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                                                                                                                                                                                                                                                                                 TITLE:
                                                                                                                                                                                                                                                                                                                             AUTHORS:
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                                                         CCATTTCTGGGCGCACATGTATCTAGCCATGGTAGCACAGGCCGGGAAGCTCTGTGCTGG 63
388-396

    Weber, James L.
    May, Paula E.
    Abundant Class of Human DNA Polymorphisms
    Which Can Be Typed Using the Polymerase Chain

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                                                                                                                        Conservative
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Kwitek, A. E.
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30.5%;
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/evidence- EXPERIMENTAL
/standard_name- "PCR primer"
/citation- ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /standard_name= "Only
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/evidence= EXPERIMENTAL
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                                                                                                                       Score 28.2; DE Pred. No. 3.1; 25; Mismatches
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RESULT 13 US-08-323-170B-1/c

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                                                                                                                                                                                                                                                                                                            Sequence 34, Application US/08162081B Patent No. 5824492
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Best Local Similarity
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                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                  APPLICANT: Bala; Waterfield, Michael John; Dhand, Ritu APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia, APPLICANT: Stefano; Gout, Ivan Tarasovitch TITLE OF INVENTION: POLYPEPTIDES HAVING KTWAGE OF SPONTON: THEIR DEFINITION OF SPONTON: THEIR DEFINITION: THEIR DEFINITIO
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4737 AATGATATCATTATCCATTAAAGCTGG 4709
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
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CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Quine, Jonathan A.
REGISTRATION NUMBER: P-41,261
REFERENCE/DOCKET NUMBER: 015280-113100US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               34 ggcccagauucgaaucuguaauaaaaguuuuuuucuucuauauccucagauuggcaguga 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER:
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149..9556
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13-OCT-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4.9%; Score 28.2;
31.5%; Pred. No. 21;
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RESULT 15
US-08-780-872-34
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Matches
                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                                                                                                                                                                                                                                                 Sequence 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 838-388 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/C
FILING DATE: February 7,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: mEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
                                                                                                                                                              NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & L
                                                                                                                                                                                                                                                                                                                                                                                                         2535 GGGACTTATTGAGGTG 2550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                    APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volini
                                                                                                                                                                                                           APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
                                                                                                               STREET: 805 Third
CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                      464 ccugcgaauuggugug 479
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STREET: 80
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              SOFTWARE:
                            COMPUTER: IBM PS, OPERATING SYSTEM:
                                                                                                    COUNTRY:
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ARE: Wordperfect APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                               Application US/08780872
                                                                                                                                                 805 Third Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3240 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                       USA
                                                                                                                                                                                                                                         Joseph; Otsu, Masayuki; Panayotou, George; Volinia, Stefano; Gout, Ivan Tarasovitch
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                                           IBM PS/2
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February 7, 1994
                                                         Diskette, 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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34.2%; Pred. No.
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                                                             360 kb storage
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FILING DATE: 09-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/162,081
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 1993
ATTORNEY/ACENT INFORMATION:
NAME: PASQUALINI, PATTICIA A.
REGISTRATION NUMBER: JUD 5256
FERENCE/DOCKET NUMBER: LUD 5256
FELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEFAX: (212) 838-3884
INFORMATION FOR SEO ID NO: 34:
SEQUENCE CHARACTERISTICS:
LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
US-08-780-872-34
Search completed: August 7, 2000, 09:28:43 Job time: 897 sec
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Page 9

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Title:
Perfect score:
Sequence:
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 1000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

O	0.0					O			Res
23	227	18	16 17	14	111	900	765	4004	Result No.
37.2 37.2 37	37.6	110.6	111 111 110.6	113	150 121	156.4	310 173.4 171	578 578 546.8 423.6	Score
	, , , , , ,	19.1	19.2 19.2 19.1	19.6	26.0	27.1	30.6	100.0 100.0 94.6 73.3	Query Match
7218 113440 70480	1143 378	160 290	160 160	180 160	887 859	51 55 55 60 65 60 65	1005	578 940 4292 1530	Query Match Length
ម ម	13	1344	444	4 81	81	81 81	818	2000	DB
I66494 AC020935 AC006973	BBU74351 AU026236	CHKSNVIC2 AU025522	CHKSNVID2 CHKSNVIF2	CHKSNVIE2 SNVLTR CHKSNVIB2	ACRLTR2 REXXX2	S/0398 S82226 S79845	RESNYA REXXXI ACRITR1	A83549 A83548 AF006065	ID
166494 Sequence 14 AC020935 Homo sapi AC006973 Homo sapi	074351 Bulweria bu	M12206 Spleen necr M12244 Spleen necr			M22224 Reticuloend V01205 Spleen necr		V01200 Spleen necr V01204 Spleen necr M22223 Reticuloend	A83549 Sequence 2 A83548 Sequence 1 AF006065 Fowlpox v	Description

Query Match Ouery Match Best Local Similarity 70.1%; Pred. No. 1.5e-163; Matches 405; Conservative 173; Mismatches 0; Indels 0; Ga Matches 405; Conservative 173; Mismatches 0; Indels 0; Ga I ggggucgccguccuacacauuguugugacgggggccagauucgaauucguaauaaaag Oy 1 ggggucgccgccacacauuguugugacgggggccaagauucguaauaaaag Db 1 GGGGTCGCCGTCCTACACATTGTTGTACGCGGGCCCAGATCCGAATCTGTAATAAAG Db 1 GGGGTCGTCTATATCCTCAGATTGGCAGTGAGAGAGAGTTTGTTCGTAATAAAAG OY 121 ggccuacuggguggggaggagauucggaagagauuuuguucgguaagacacacauuugg OY 121 ggccuacuggguggggaggguccggacugaauccguaguauucgauacaacacuuugg OY 121 ggccuacugggugggguaggguccggacugaauccguaguauucgauacaacacuuugg OY 121 ggccuacuggggugggguacggacgaacucggaauccguaguauucgaacacacuuugg OY 181 gggcucggcgggauuccuccccaacggcaacagaagugccuacuucucgaacuccggc OY 181 gggcucggcggauuccucccccaacggcaagaggccuacuguuucucgaacuccggc OY 181 gggcucggcaggauccucccccaacggcaaagugccuacguacucuccggc OY 181 gggcucggaaguacuccucccccaacggcaaagugccucagaacucuccaggc OY 181 gggcucggaagaaguacucucccccaacggcaaaagugccucagaacuccuccaggc OY 181 gggcucggaaguaaguacucucccccaacggcaaaagugccucacggccaacaccuccaggcaacaccucggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccagaagugccuccuccagaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccaggcaacaccuccagacacaccacacaca	ALIGNMENTS AB3549 578 bp DNA A83549 1 GI:6732808 IION A83549 1 GI:6732808 US Reticuloendotheliosis virus Viruses; Retroid viruses; Retroviridae; retroviruses; 3-Reticuloendotheliosis vi ENCE 1 (bases 1 to 578) HORS HOYEL INTERNAL RIBOSOME ENTRY SITE AND VE REAL PATENT: WO 9849334 A 05 NOV-1998; RRAL GABUS DARLIX CAROLINE (FR); INST NAT SAN RES 1.578 GABUS DARLIX CAROLINE (FR); INST NAT SAN LOCATION (VALUE OF A) //Organism-"Reticuloendothelios: //Strain-"TYPE A (REV-A) //db_xref-"taxon:11636" COUNT 94 a 139 c 172 g 173 t	25 36.4 173618 57 AC019045 26 36.4 6.3 1143 4 AP076053 27 36.2 6.3 2041 12 MUSENZEIA 28 36 6.2 16832 42 AC014255 28 36 6.2 114958 51 AC008356 29 36 6.2 114958 51 AC008354 20 31 36 6.2 114958 51 AC008234 20 31 36 6.2 1151820 40 AL157931 31 35.8 6.2 151820 40 AL157931 32 35.8 6.2 186518 60 AC016813 35.8 6.2 10264 4 MUPACYT21 26 37 35.2 6.1 176043 77 AC027072 27 38 35.2 6.1 213721 10 HSD762504 28 34 36 6.0 168613 40 AL139318 29 34.6 6.0 168613 40 AL139318 20 34.6 6.0 168613 40 FHUS9841 34.6 6.0 167656 31 AD031645 34.6 6.0 167656 31 AD031615 34.4 6.0 68734 51 AC027171
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Conservative 173; Mismatches 0; Indexs 0; Indexs 0; Indexs 0; Indexs 0; Indexs 1;	RESULT 2 A83548 A83548 A83548 DEFINITION Sequence 1 from Patent WO9849334. A83548 ACCESSION A83548 ACCESSION A83548.1 GI:6732807 VERSION RETWORDS SOURCE ORGANISM TITLE ORGANISM TITLE JOURNAL AUTHORS SOURCE SOURCE JOURNAL AUTHORS SOURCE JOURNAL AUTHORS SOURCE JOURNAL AUTHORS AUTHORS SOURCE JOURNAL ADDES JOURNAL ADDES JOURNAL	241 GCCGGTAAGTAAGTACTTGATTTTGGTACCTCGCGAGGGTTTGGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGATCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGA

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sequences. from the avian retrowrus. Teliculoendotheliosis viruslogy 235 (2), 367-376 (1997)
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49. .900
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PVRKSGTSEYRWYQLLEVKRKVETIHFTVPNPYTLLSLLPPDRIWYSVLDLKDAFFC
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O'Rear J.J. and Temin, H.M.

Spontaneous Changes in nucleotide-sequence-in-proxicuses necrosis virus, an avian-retrovirus

Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-1234 (1982)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shimotohno, K., Mizutani, S., and Temin, H.M. Sequence of retrovirus provirus resembles that of transposable elements.

Nature 285 (5766), 550-554 (1980)
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Spleen necrosis virus.
Spleen necrosis virus
Spleen necrosis virus
Viruses; Retroviridae; Mammalian
Viruses; Retroid viruses; Retroviridae; Mammalian
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383
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/db_xref="taxon:11836"
313
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                                                                                              /db_xref="Swiss-prot:p03342"
/translation="McQAGSKGLLTPLECTIKNFSDFKKRAGDYGEDVDSFALRKLCE/translation="McQAGSKGLLTPLECTIKNFSDFKKRAGDYITITWTDITIERFKYLKSCLEWPTFGVORPKEGTLDFKVVAAVRAIVFGRPGHPDQVIYITWTDITIERFKYLKSCGCKPHRTSKVLLASQKVNPRRPVLPSAPESPPRIRRAGFLDERFLSPAPAPPPPPPESAIVEDTREGQDDSTYMTSPPHTRSGLEFGAQGFSGMYPLRETGERDMTGRPMRTYVPFTTSDLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSSLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNQNPSSFSQAPDQVISLLESVFYTHQPTWDDCQQULRTLFTTEERER VRITSPLYMKNGNPSSFAPDWVGS
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/note="G is
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/db_xref="GI:61758"
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Shimotohno, K.,
                              Spleen necrosis virus.
Spleen necrosis virus
Viruses; Retroid viruses;
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Spleen necrosis virus
V01204 J02388 M12296
V01204.1 GI:61793
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       Mizutani, S. and Temin, H.M.
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                     Retroviridae; Mammalian type C virus group.
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Reticuloendotheliosis virus 713 proviral clone RNA.
M2223 M10659 M16722
M2223.1 GI:209708
long terminal repeat (LTR).
Reticuloendotheliosis virus (from chicken line 151-5 B
CDNA to mRNA, clone 713.
Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian type
retroviruses; 3-Reticuloendotheliosis virus group.
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Nature 285 (5766), 550-554 (1980)
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/db_xref="taxon:9036"
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/db_xref="taxon:9036"
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/db_xref="taxon:11836"
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/db_xref="taxon:11836"
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                                                GenBank staff at the National Library of Medicine created this entry [NCBI glbbsq 148190] from the original journal article. This sequence comes from Fig. 3.
Location/Qualifiers
1. .545
                                                                                                                                      Structural genes, not the LTRs, are the primary reticuloendotheliosis virus A-induced runting ar virology 202 (1), 116-128 (1994)
                                                                                                                                                                                    Filardo, E.J., Lee, M.F. and Humphries, E.H.
                                                                                                                                                                                                                  Reticuloendotheliosis virus A.
Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian
retroviruses; 3-Reticuloendotheliosis virus group.
                                                                                                                                 94279132
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87226389
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B-lymphoma induction by reticuloendotheliosis Characterization of a mutated chicken syncytia involved in c-myc activation
J. Virol. 61, 2084-2090 (1987)
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In vitro transcription analysis of the viral promoter involved comyc activation in chicken B lymphomas: Detection and mapping comyc activation sites within the reticuloendotheliosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 67.2
31; Conservative
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J. Virol. 54, 161-170 (1985)
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 /organism="Reticuloendotheliosis
/db_xref="taxon:11636"
119 c 144 g 149 t
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/db_xref="taxon:11636"
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Pred. No. 1.6e
57; Mismatches
9
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6;
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nal repeats, pro-
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NA, 545 nt
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                     126;
   gggcuc 186
                                                                                                                                                 122;
                                                                                                                                                                                                                                                                                                                     viruses; dsDNA viruses, no RNA stage; Herpesviridae.

1 (bases 1 to 585)

Jones, D., Brunovskis, P., Witter, R. and Kung, H.J.

Retroviral insertional activation in a herpesvirus: transcriptional activation of U(S) genes by an integrated long terminal repeat in a Marek's disease virus clone
J. Virol. 70 (4), 2460-2467 (1996)

96183893
                                                                                                                                                                                                                                                                                                                                                                                                                                                    S82226 585 bp {RS region, intervening Genomic DNA, 585 nt].
                                                                                                                                                                                                                                                                   GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 178131] from the original journal article. This sequence comes from Fig. 1C.

Authors indicate intervening sequence from nt 23 to nt 555 inclusive derived from co-infecting reticuloendotheliosis virus
                                                                                                                                                                                                                                                                                                                                                                                                       Gallid herpesvirus 2 RM1. Gallid herpesvirus 2
                                                                                                                                                                                                                                                                                                                                                                                                                                 S82226.1 GI:1839499
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S82226
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26; Conservative
                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                              CSV
                                                                                                                                                                                                           /organism="Gallid herpesvirus
/db_xref="taxon:10390"
125 c 162 g 155 t
                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29.6%; Score 171; DB 81; Length 68.9%; Pred. No. 8.7e-41; tive 56; Mismatches 0; Indels
                                                                                                                                                          27.1%;
                                                                                                                                                 52;
                                                                                                                                                 Score 156.4; DB bi,
Pred. No. 2.2e-36;
Pred. No. 2.2e-36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ONA VRL sequence] [Marek's C
                                                                                                                                                                    DB 81; Length 585;
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journal article
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Matches 118
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Reticulcendotheliosis virus 71

M2224 M10660 M16722

M22224.1 GI:209709

long terminal repeat (LTR).

Reticulcendotheliosis virus (f
cDNA to mRNA, clone 713.

Reticulcendotheliosis virus

Reticulcendotheliosis virus
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118; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank staff at the National Library of Medicine created this entry [NCBI gibbsq 79845] from the original journal article. This sequence comes from Fig IC.
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                                                     viruses; Retroid viruses; Retroviridae; Mammalian type C retroviruses; 3-Reticuloendotheliosis virus group.

1 (bases 510 to 602)
Ridgway, A.A., Swift, R.A., Kung, H.-J. and Fujita, D.J.
Ridgway, A.A., Swift, R.A., Kung, H.-J. and Fujita, D.J.
In vitro transcription analysis of the viral promoter involved in vitro transcription analysis of the viral promoter involved in the cativation in chicken B lymphomas: Detection and mapping C two RNA initiation sites within the reticuloendotheliosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Viruses; dsDNA viruses,
1 (bases 1 to 583)
long terminal repeat
J. Virol. 54, 161-170 (1985)
85135063
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/insertion_seq=""
/db_xref="taxon:10390"
/db_xref="taxon:10390"
145 c 123 g 149 t
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1. .583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 153; DB 81;
Pred. No. 2.3e-35;
55; Mismatches 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   no RNA stage; Herpesviridae
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                                                                                                                                                                                                                                                   chicken line
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                                                                                                                                                                                                                                                                                                                                  clone RNA.
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                                                                                                                                                                                                                                                       151-5 B lymphomas),
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Spleen necrosis virus
Spleen necrosis virus
Viruses; Retroid viruses; Retroviridae; Mammali
retroviruses; I-Mammalian type C virus group.
1 (bases I to 859)
Shimotohno, K., Mizutani, S. and Temin, H.M.
Sequence of retrovirus provirus resembles that
transposable elements
                                                                                                                                                                                                                                                                                                                                                         REXXX2 859 bp
Spleen necrosis virus
V01205 J02389
V01205.1 GI:61794
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Reticuloendotheliosis virus"
/db_xref="taxon:11636"
246. 750"
/note="3' LTR"
eature 805. 806
/note="cryptic intron splice donor site
212 a 216 c 227 g 232 t
About 700 bp after segment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Characterization of a mutated chicken syncytial virus provirus involved in c-myc activation J. Virol. 61, 2084-2090 (1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               B-lymphoma induction by reticuloendotheliosis virus:
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Swift,R.A., Boerkoel,C.F., Ridgway,A., Fujita,D.J., Dodgson,J.B.
                                                                          245
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                         285
                                                                          ø
                                                                                                                                                                  /organism="Spleen necrosis virus"
/db_xref="taxon:11836"
<1. .740
                                                                   /note="cellular DNA"
/organism="Spleen necrosis virus"
/db_xref="taxon:11836"
199 c 214 g 201 t
                                                                                                                    /proviral
/db_xref="taxon:11836"
741. .>859
                                                                                                                                                                                                               Location/Qualifiers
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1. .887
                                                                                                                                                                                                                                    (5766), 550-554 (1980)
             20.9%;
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    48;
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                                                                                                                                                                                                                                                                                                                                                                        S (3'
             Score 121; DB 81;
Pred. No. 1e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 150; DB 81;
Pred. No. 1.9e-34;
53; Mismatches 10;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                             NA VRL 06-APR-1 end) integrated in chicken cell.
   10;
                                                                                                                                                                                                                                                                                                        Mammalian
                       Length 859;
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CHKSNVIE2
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                                                                                                                                                                                                              CGGACTGAATCCGTAGTACTTCGGTACAACATTT 152
                                                                                                                                                                                                                                                            1 (bases 1 to 180)
Iwasaki,K. and Temin,H.M.
The efficiency of RNA 3'-end formation is determined by the distance between the cap site and the poly(A) site in spleer necrosis virus
                                                           Spleen necrosis virus.
Spleen necrosis virus
Viruses; Retroid viruses;
Tetroviruses; 1-Mammalian
                                                                                                                     X59450.1 GI:61992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shimotohno, K. and Temin, H.M.
Evolution of retroviruses from cellular |
Cold Spring Harb. Symp. Quant. Biol. 45,
81259597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves: Neoqnathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Chicken DNA and proviral spleen necrosis
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Spleen necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         integration site; proviral gene. 2 of 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             M12248.1 GI:212691
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4.5 kb downstream of segment 1.
                                                                                                                                             180 bp
necrosis virus
                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Gallus gallus"
/db_xref="taxon:9031"
31 c 47 g 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                         19.7%; Score 113.6; DB 4; 63.6%; Pred. No. 1.8e-23; tive 44; Mismatches 9;
                                                                                                                                             DNA
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proviral DNA/chicken
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                                                        Retroviridae; Mammalian
type C virus group.
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CHKSNVIB2
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polyA_site
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                                                    145
                                                                                                                                                                                                                                                                                                  y Match 19.3%; Score 111.6; DB 4; Local Similarity 63.1%; Pred. No. 7.2e-23; hes 101; Conservative 42; Mismatches 14;
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| CTGGCCTACTGGGTGGGCGCAGGG 163
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                             | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 1990 | 
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90; Conservat
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/db_xref="taxon:9031"
36 a 33 c 47 g 44 t
About 4.5 kb downstream of segment 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            integration site; proviral gene. 2 of 2
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M12242.1 GI:212682
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Spleen necrosis virus proviral DNA/chicken DNA (clone 60),
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Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
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/db_xref="taxon:11836"
/clone="pSNV(wt)"
<1. >180
/note="LTR"
74. 79
102.
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1. .180
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; Pred. No. 2.7e-23;
42; Mismatches 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58
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RESULT 15
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TITLE
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145
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                                                  cggacugaauccguaguauuucgauacaacauu 177
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M12246
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Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Archosauria;
Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 160)
Shimotohno, K. and Temin, H. M.
Evolution of retroviruses from cellular movable genetic elements
Cold Spring Harb. Symp. Quant. Biol. 45, 719-730 (1981)
81259597
                                                                                                                                                            ch 19.2%; Score 111; DB 4; 1
1 Similarity 64.1%; Pred. No. 1.1e-22;
98; Conservative 42; Mismatches 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          integration site;
                                                                                                                                                                                                                           /organism="Gallus gallus"
/organism="Gallus gallus"
/db_xref="taxon:9031"
46 g 46
34 a 34 c 46 g 46
: 4.5 kb downstream of segment
                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .160
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Human IL-1ra BAC c Partial Factor VII Factor IX/Factor V Factor IX/Factor Coprinus cineraus Entercoccus faeca Entercoccus BAC c Human IL-Ira BAC c Human Sis SCAREC Arabidopsis SCAREC Kidney Injury asso Kidney Injury asso Allergen Alt a 12 NA encoding a kri DNA encoding a kri DNA encoding a kri DNA encoding a kri

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GGACGCUGCCGGGAAGCUCCACCUCCGCUCAGCAGGGGACGCCCUGAUCUGAGCUCUGUG

В В γQ 밁 Ş д PD 30-OCT-1993.

PP 28-APR-1997; 005203.

PA (INRM) INSTEM INST MAT SANTE & RECH MEDICALE.

PI DATILY JL, Gabus Datritx C, Lopez LM;

PI Expression vectors containing IRES and/or encapsidation enhancer
Expression vectors containing IRES and/or encapsidation enhancer
CC The present sequence is derived from the 5' end of the genomic RNA of a type C retrovired from the 5' end of the genomic RNA of a type C retrovire of the Jr Part of the 5' derived sequence are used as an internal ribosome entry site of crecombinant polypeptides or enhancing the encapsidation of a recrowing polypeptides or production of transgenic animals.

PS Sequence 940 BP; 190 A; 225 C; 260 G; 265 U; δã Query Match
Best Local Similarity 100.0%; Score 578; DB 1; Length 940;
Matches 578; Conservative 0; Mismatches 0; Indels 543 GGGCUCGUCGGGAUUCCCCCCAUCGGCAGAAGUGCCCUACUGUUUCGUCGGAACUCCGGC 602 181 gggcucguccggggauuccuccccaucggcagaagugccuacuguuucuucgaacuccggc 240 483 deccuacuedes de decedence de la cue de decedencia de la cue de 121 ggccuacuggguggguagggguccggacugaauccguaguauuucgauacaacauuugg 180 363 GGGGUCGCCUACACAUUGUUGUGACGCGCGGCCCAGAUUCGAAUCUGUAAUAAAAG 422 61 uuuuuucuucuauauccucagauuggcagugagaggagauuuuguucgugguguaggcu 120 1 9999ucgccguccuacacanuguugucgcgcgggcccagauucgaaucuguaauaag 60 17-MAR 1999 (first entry)
Sequence derived from the 5,
Reticulcendotheliosis virus type A; REV-A,
retrovirus; internal ribosome entry site; IRES, encapsidation;
Reticulcendotheliosis virus.
Reticulcendotheliosis virus.
Reticulcendotheliosis virus. V63778 standard; DNA; 940 BP. 481 CCACACCGCGCGCGCGUGCGAAUAAUACUUUGGAGAGUCUUUUGGCCUCCAGUGUCUGCGGU 0,

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Db 1591 GGGCTCGCCGTCCTACACATTGTTGTGACGTGCGGCCCAGATTCGAATCACAAAG 1650 1:::::::::::::::::::::::::::::::::::	De 603 CCCCIONACIDADUCADUCUCADUCUCACUCACIONACIDADUCACUCA PROPERMINANTALITA SE ANDREAS PROPERMINANTALITA	į
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                                                                                                                     Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and form provirus

From the page 17; 28pp; English.

The universal retroviral vector pPoll5-R1 (given in 076041) was obtained by replacing the SV40 promoter and hpt gene of pPoll1-R1 (Q76038) with the multiple cloning site of pBluescript II KS. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 3878 Bp; 922 A; 948 C; 988 G; 1020 T;
                                                                                                                                                                                                                                           07-JUN-1994; U06415.
07-JUN-1993; US-073345.
(UYNE') UNITA-NEW JERSEY.
Dornburg RC;
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                                        684
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58 aaguuuuuuucuucuauauoccucagauuggcagugagaggagauuuuguucgugguguag
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                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                            entry)
                                                                      72.2%; Score 417.4; DB 1; 64.0%; Pred. No. 3.5e-126; Live 160; Mismatches 31;
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                                                                                                                                                                                                                                                                                                                   spleen necrosis virus;
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                                                                      Indels
                                                                                          Length 3878;
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RESULT OF THE PT ACCOUNT ACCOU
                     Query Match
Best Local S
Matches 381
                                                                                                            Tability to produce progeny virus, in helper cell which can infect in strong tell and form provirus and produce progeny virus, in helper cell which can infect is Example; Page 16-17; 28pp; English.

New recombination-free, highly efficient retroviral vectors (ppolli-R1 (given in 076038), ppolli-R2 (076039) and ppolli-R3 (076040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5519 BP; 1264 A; 1420 C; 1456 G; 1379 T;
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20-JUL-1995 (first entry)
20-JUL-1995 (first entry)
Retrovirus vector pP0111-R3; spleen necrosis virus; SNV;
Retrovirus; vector; pP0111-R3; spleen necrosis virus; SNV;
Cytomegalovirus; CMV; intermediate-early promoter; IE prom
                                                                                                                                                                                                                                                                                                                                                                     Recombinant retrovirus vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                       22-DEC-1994. U06415. 07-JUN-1994; US-073345. (UYNE-) UNIV NEW JERSEY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy; ss.
Spleen necrosis virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Dornburg
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         Score 410; DB
Pred. No. 1.1e
51; Mismatches
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DB 1,
1.1e-123;
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161;

Length Indels

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D2-DEC-1994.

D2-DEC-1994; U06415.

PF 07-JUN-1994; U06415.

PF 07-JUN-1993; US-073345.

NOTUN-1993; US-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; PS-073467/05.

NOTUN-1994; US-073467/05.

NOTUN-1994; US-07467/05.

NOTUN-
                                                                                                                                                                                                                                                                            cytomegalovirus; CMV; intermediate-early promoter; IE promoter; long terminal repeat; LTR; encapsidation; gene transfer; spleen necrosis virus.

Spleen necrosis virus.

W09429437-A.
22-DEC-100.
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Evalpox virus (FPV M5) LTR sequence.
DE Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV.
KW vaccine; chicken; LTR; long terminal repeat; ss.
V vaccine; chicken; LTR; long terminal repeat; ss.
Fowlpox virus.
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08-AUG-1997; AU-008454.
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pr occurrence in chickens; English.

English 18; Fig rates to a recombinant fowlpox virus (REV), and so related to a recombinant fowlpox virus virus (REV), and so recall does not related to reticuloendotheliosis virus that the recombinant FPV is recall does not encode an active reticuloendothe. The recombinant FPV is red does not contain any Exp sequence. The vaccine is used to ground does not contain any Exp sequence. The recombinant FPV is call does me does not contain any Exp sequence to thickens older than contain the contain any experiment to vaccine is deer than contained with the vaccine subsequent to vaccine and field strains of vaccinated at older than 1 day of age. Alternatively strains carry a vaccinated at older than 1 day of age. Prior vaccine and field strains of vaccine provides the respectation of the reverse of the reverse of the reverse and when chickens are infected. The represent from the containation provides the means by which a x26110-115 represent reverse the means by which a x26110-115 represent reverse the means by which a x26110-115 represent reverse to the new respectation of the new r
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20-MAY-1999 (first entry)
Chicken syncytial virus provirus REV LTR sequence.
Chicken syncytial recombinant; reticulcendotheliosis virus; pry; recombinant; reticulcendotheliosis virus.
Fowlpox virus; pry; recombinant repeat; ss.
Fowlpox virus; long terminal repeat; ss.
Veccine; chicken; LTR; long terminal repeat; ss.
Avian reticulcendotheliosis virus.
Avian reticulcendotheliosis virus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O7-AUG-1998; AU-008454. 6 IND RES ORG. O7-AUG-1997; AU-008454. 6 IND RES ORG. O8-AUG-1997; AU-008ALTH SCI 6 IND RES ORG. OS. AUG-1997; COMPAT BEH, Gould AR, Hert19 BOYLE DB. COMPAT BEH, Gond AR, Hert19 BOYLE DB. COMPAT BEH, Gond AR, Hert19 BOYLE DB. COMPAT BEH, GOND ARTHUR WEI; 99-167426/14.
                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 99-167428/14. against fowlpox virus - is free of contamination Recombinant vaccine against fowlpox virus - is free of contamination recombinant vaccine against fowlpox virus, used to prevent the virus from reticuloendotheliosis virus, used to prevent the virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27.28;
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%; pred No. 1.1e:
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L.1e-41
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В
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                                                                                                                                                                                                                                                                                                                                    PT New isolated nucleic acid encoding plant ADA2 transcription activator used for regulating expression of genes in plants and to free for specific inhibitors, potentially useful as herbicides of from phaseous sequence encodes the ADA2 transcription adapter isolated for sequences. Transfecting cells which characterized are chimeric genes comprising of a the ADA2 nucleic acid sequence operably linked to suitable regulatory to reduce expression of particularly to reduce expression of particular genes can be used: (1) to compare the following protein, compared by factors with which ADA2 includes protein, compared by factors with which ADA2 increase protein, compared by factors with which ADA2 interact; and (ii) to compare the ADA2 nucleic acid sequence or suppression of genes containing promoters or to incompounds that inhibit ADA2, potentially useful as herbicides. The ADA2 nucleic acid sequence (or synthetic primers based or mapping genes (e.g. for plant breeding) or to identify promoters for mapping genes (e.g. for plant breeding) or to identify loss of function sequence is 1812 Bp; 613 A; 318 C; 404 G; 477 T;
                                                                                                                                                                                                           Query Match
Best Local Similarity 34.98; Score 33; DB 1; Length 1812;
Matches 45; Conservative 24; Mismatches 60; Indels
373 GAAGAGATGTTACTTCTAGAGGCCATTGAGATGTATGGATTCGGGAAGGGGAATGAAGTT 432
                                                                                              313 CCGTATCGGATTATGGATAATCTATCTTTTTCCACTTATATGTCCAGATTGGAATGCAGAT 372
                                        97 gaganunuguucgugguguaggcuggccuacugggugggguagggguccggacugaaucc 156
                                                                                                                                    γQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 99-132248/11.
P-PSDB; W99017.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Phaseolus lunatus ADA2 transcription adapter encoding cDNA.

Reseolus lunatus, ADA2; transcription adapter encoding cDNA.

Reseolus lunatus.

Accation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 26.9%; Score 155.4; DB 1;
Matches 117; Conservative 53; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X18925 standard; cDNA; 1812 Bp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 uuuuuuucuuucuauauccucagauuggcagugagaggagauuuuguucgugguguaggcu 120
397 -CTTTTTCTTCTATATCCTCAGATTGGCAGTGAGAGGAGATTTTGTTCTTGTGCTGGCT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             337 dederneed de la commencia del commencia del commencia de la commencia de la commencia del commen
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Sequence 512 BP; 130 A; 113 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 9999ucgccguccuacacauuguugugacgcgcggcccagauucgaaucuguaauaaag 60
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162570/c
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Best Local S
Matches 23
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05-JUL-1995; JP-191028.
(SAPB) SAPPORO BERMERIES.
Ito K, Kihara M, Okada Y,
WPI: 97-108966/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          23-JAN-1997.
05-JUL-1996; J01866.
05-JUL-1995; JP-191028.
(SAPB ) SAPPORO BREWERIES.
Ito K, Kihara , Okada Y,
Expression promoter for genes inserted into plant seeds - e.g. heat-resistant beta-amylase gene inserted into barley seeds

Example 6; Page 20-21; 33pp; Japanese.

T62572 is a DNA molecule comprising a heat resistant promoter derived from a barley beta-amylase (EC 3.2.1.2) gene and other sequences used for integration of this promoter into a reporter plasmid. The plasmid is used for the production of transgenic barley plants and seeds. Such plants and seeds have improved maturation properties. Sequence 2142 BP; 651 A; 482 C; 395 G; 614 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Barley;
plant; j
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23-JAN-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare.
WO9702353-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expression promoter for genes inserted into plant seeds - e.g. heat-resistant beta-amylase gene inserted into barley seeds claim 5; Page 17-18; 33pp; Japanese.
T62570 is a heat resistant promoter derived from a barley beta-amylase (EC 3.2.1.2) gene. The promoter is used for the production of transgenic barley plants and seeds. Such plants and seeds have improved maturation properties.
Sequence 1276 BP; 393 A; 237 C; 234 G; 412 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T62572 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Heat-resistant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hordeum vulga:
WO9702353-A1.
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Heat-resistant barley beta-amylase gene promoter.
Barley; heat resistant; promoter; genetic engineering; transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     esistant barley beta-amylase gene promoter containing; heat resistant; promoter; genetic engineering; transimproved maturation; ds.
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Pred. No. 2.6;
8; Mismatches
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Query Match
Best Local S
Matches 23
                                                                                                                                          23 AUG-1985; 306017.

24-AUG-1984; US-644306.

06-NOV-1984; US-668764.

26-JUL-1985; US-788517.

(UPJO) UPJOHN CO.

Goodwin EC, Palermo DP, I
Disclosure; Page 5; 32pp; English.
This cattle growth hormone sequence is part of recombinant DNA which is especially useful for expression of tissue plasmingen-activator.
Sequence 2205 BP; 432 A; 616 C; 702
                                                                   New recombinant DNA for polypeptide expression cells - contg. poly:adenylation signal, coding selection marker
                                                                                                       N-PSDB; N60157.
                                                                                                                                                                                                                       05-MAR-1986
                                                                                                                                                                                                                                       EP-173552-A
                                                                                                                                                                                                                                                              polya_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Somatotropin; growth hormone;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cattle growth
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N60157;
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n hormone (somatotropin)
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1089 . 1317
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1480 . 1754
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1754 . 1954
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746. .971
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585
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337. .584
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                                                                                                                                          Rottman
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                     a circular
the high-yield
 <u>ن</u>
                                                                       in eukaryotic
gene, promoter
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Best Local Similarity
Matches 54; Conserv
                                                                                                                                                     P-112012-A.

Depth 12012-A.

D
Query Match 5.3%; Score 30.6; DI
Best Local Similarity 43.2%; Pred. No. 3.4;
Matches 54; Conservative 12; Mismatches
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N40081;
04-FEB-1992 (first entry)
Sequence of genomic bowine growth hormone (BGH).
Growth promoter; hormone; lactation; ss.
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nilarity 43.2%;
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259 gauuuugguaccucgcgaggguuugggaggaucggaguggcgggacgcugccgggaagcu 318

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Db 739 GAGTTTGTAAGCTCCCGAGGATGCGTCCTAGGGTGGGGAGGCAGGAAGGGGTGAATCC 798

Qy 319 ccaccuccgcucagcaggggacgcccugaucugagcucugugguaucugauuguugg 378

Db 799 ACACCCCTCCACACAGTGGGAGGAAACTGAGGAGTTCAGCCGTATTTTATCCAAGTAGG 858

Qy 379 accgu 383

Db 859 GATGT 863
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Search completed: August Job time: 458 sec

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Page 9

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Title:
Perfect score:
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Maximum Match 100%
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Maximum DB seq length: 1000000
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Gapop 10.0 , Gapext 1.0
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652.183 Million cell updates/sec
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SUMMARIES

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164655 187883 193315 196124 1961284 101584 109003 115402 149466 175399

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448 146956 174191 192651 198381

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1 (bases 1 to 578)
Gabus-Darlix,C. and Darlix,J.
GABUS-DARINAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING
PATENT: WO 9849334-A 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
LOCATION/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                     Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian type
retroviruses; 3-Reticuloendotheliosis virus group.
                                                                                                                                                                                                                                                        /organism="Reticuloendotheliosis
/strain="TYPE.A (REV-A)"
/db_xref="taxon:11636"
/db_xref="taxon:11636"
139 c 172 g 173 t
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; Pred. No. 6.3e-85;
93; Mismatches 0;
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Matches 221; Conserv
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|CCGGCCGGGATGGG 578
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                                                                                                                                                                                  CCGCCCGGGATGGG
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Gabus-Darlix,C. and Darlix,J.
GABUS-DARLIX,C. and DARLIX,J.
HOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING
PATENT: WO 9849334-A 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A83548 94
Sequence 1 from
A83548
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Reticuloendotheliosis virus
Reticuloendotheliosis virus
Viruses; Retroid viruses; Retroviridae; Mammalian type
retroviruses; 3-Reticuloendotheliosis virus group.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A83548.1
          Fowlpox virus.
Fowlpox virus
Viruses; dsDNA
                                                          ArU06065 4292 bp DNA Fowlpox virus S gag gene, cc (pro/pol) gene, partial cds. AF006065
                                                    AF006065.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                       190
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Reticuloendotheliosis
/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENO
/db_xref="taxon:11636"
/db_xref="taxon:11636"
1 225 c 260 g 265 t
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               dsDNA viruses,
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                                                     GI:2393892
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                                                                                                                                                                                                                                                                                                                                                                                          %; Score 314; DB 5;
; Pred. No. 6.5e-85;
93; Mismatches 0;
               no RNA
                                                                                   complete
               stage;
                                                                                     cds,
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                 Poxviridae;
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                  Chordopoxvirinae;
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RESULT 1
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A83549

578 bp om Patent

Sequence 2 from 1 A83549 A83549.1 GI:6733

GI:6732808

REFERENCE AUTHORS TITLE

FEATURES

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BASE COUNT ORIGIN

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325

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Query Match Best Local S Matches 221

Similarity

100.0%;

221;

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241

445 181 385 121 SOURCE ORGANISM VERSION KEYWORDS

Reticuloendotheliosis virus.

JOURNAL MEDLINE REFERENCE AUTHORS TITLE

FEATURES

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REFERENCE AUTHORS

TITLE

1562

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tch 96.9%; Score 304.4; DB 82; al Similarity 68.5%; Pred. No. 5.8e-82; 215; Conservative 93; Mismatches 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (30-MAY-1997) Division of Animal Health, CSIRO, Portarlington Road, Geelong, Victoria 3213, Australia Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l (bases 1 to 4292)
Hertig,C., Coupar,B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virus 97428585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hertig, C.H., Coupe
Direct Submission
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                                                                                                                                                                                                                                                                                                                                         /product="protease/polymerase"
/protein_1d="AAC58240.1"
/db_xref="Gi:2393895"
/db_xref="Gi:2393895"
/translation="GROGSSALREPRLKVKVGGQIIDFLVDTGATHSVVQKEVGPMSK
ESVAIIGATGNIRNYPKSEGRLVDLGRGLVTHSFLVIPECPDPLLGRDLLQKLRATIS
ETGEGPEDIRTECKLLVTAPLEEEYRLFLEAPIQNVTLLEQWKREIPKVWAEINPPGL
ASTQAPIHVQLLSTALPVRVQYPITLEAKRSLRETIRKFRAAGIIAPVHSPWNTPLL
PVRKSGTSEYRWQDLAEVURGVETHPTVPNPYTLLSLLPPDRIWYSVLDLKDAFFC
IPLAPESQLIFAFEWADAEEGESGQLTWTRLPQGFKKSPTLEDEALNRDLQ"
a 973 c 1064 g 1051 t
                                                                                                                                                                                                                                                                                                     /gene="pro/pol"
<3312. .>4292
                                                                                                                                                                                                                                                                                                                      RGSKKTPPGKGRPPLGKNQCAYCKEEGHWKKNCPKLVSGATPVLVEELQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="gag"
1812. .3311
/gene="gag"
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                                                                                                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/product="hypothetical protein"
/protein_id="AAC58238.1"
/db_xref="GI:2393893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Strain="S (standard vaccine strain)"
/db_xref="taxon:10261"
/note="standard vaccine strain from Cyanamid-Webster
Ltd, Castle Hill, New South Wales, Australia.
ECORI/PstI 4.3kb fragment from the 9.8kb PstI genome
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                               Indels
                                                         Length
                                                         4292;
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                           Gaps
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Spontaneous changes in nucleotide sequence in proviruses necrosis virus, an avian retrovirus
Proc. Natl. Acad. Sci. U.S.A. 79 (4), 1230-1234 (1982)
                                                                                                                                                                                                                                                                                                                         The meaning of the substitution at 739-749 is not completely clear
                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases_2_to_4.70).

Shimotono,K., Mizutani_S_and Temin,H.M.

Sequence of retrovarus provirus resembles that of bacterial transposable elements

Nature 285 (5766), 550-554 (1980)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Integration site; provirus; terminal Spleen necrosis virus. Spleen necrosis virus Viruses; Retroid viruses; Retrovirida
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V01200.1 GI:61757
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                  /note="C
375
                                              /note="C
374
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327
                                                                          /note-"A
374
                                                                                                                                  /note="T is missing 367
    'note="T
                                                                                                                    /note-"G
                                                                                                                                                                                                                         /note="T is missing in clone 13"
                                                                                                                                                                                                                                                          /organism="Spleen necrosis virus"
/db_xref="taxon:11836"
                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Query Match Best Local S Matches 215

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383
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891 bp
necrosis virus
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/db_xref="SWISS-PROT: P03342"
/tamslation="MGQAGSKGLLTPLECILKNESDFKKRAGDYGEDVDSFALRKLCE
/translation="MGQAGSKGLLTPLECILKNESDFKKRAGDYGEDVDSFALRKLCE
/translation="MGQAGSKGLLTPLECILKNESDFKKTAGTLDERPLSPAYAPPPPYPEV
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SAIVEDTREGQQPDSTVWTSPPHTRSGLEFGAQGPSGMYPLRETGERDMTGRPMRTYV
PATTSDLYNWKNONPSSFSQAPDQVISLLESVFYTHQPTWDDCQQLLRTLFTTEERER
PRTESRREVRNDQGVQVTDEREIEAQFPATRPDWVGS"
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/db_xref="GI:61758"
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  DNA VRL 06-APR-1993 (5' end) integrated in chicken cell.
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875 GTTCGTCGTTTGTCGAC
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Spleen necrosis virus
Viruses; Retroviridae; Mammalian
Viruses; Retroviruses; 1-Mammalian type C virus group.
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V01204.1 GI:61793
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Shimotohno,K., Mizutani,S. and Temin,H.M.
Sequence of retrovirus provirus resembles
transposable elements
transposable elements
(1980)
                                                                                                                                                                             290 bp DNA
Rattus norvegious, OTSUKA clone,
sequence, sequence tagged site.
AU0355522
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity 64.
26; Conservative
Watanabe, T.K., Hishigaki, H., Kanemoto, N., Miyakita-Mizoguchi, A., Oga, K., Okuno, S., Ono, T., Tsuji, A., Hayashi, H., Adachi, M., Yamasaki, Y., Iriye, Y., Takahashi, E., Takagi, T., Nakamura, Y. and Tanigami, A.
The large-scale mapping of rat microsatellite markers
Unpublished (1998)
2 (bases 1 to 290)
                                                                                                      Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                           Rattus norvegicus DNA, clone:0T29.32/731c09
                                                                                                                                                                        AU025522.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Gallus sp."
/db_xref="taxon:9036"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Spleen necrosis
/db_xref="taxon:11836"
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/db_xref="taxon:11836"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /proviral
/db_xref="taxon:9036"
215 c 246 g
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                                                                                                                                                                          GI:4515445
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OT29.32/731c09,
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Best Local Similarity 29.8
Matches 37; Conservative
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Best Local S
Matches 37
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                                                                                                                                                                                                                                                                                                 Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databases. Takeshi K Watanabe, Otsuka Pharmaceutical Co., Ltd.; Otsuka GEN Research Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, Tokushima 771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp, Tel:81-886-65-2888, Fax:81-886-37-1035)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Watanabe,T.K., Hishigaki,H., Kanemoto,N., Miyakita-Mizoguchi,A., Oga,K., Okuno,S., Ono,T., Tsuji,A., Hayashi,H., Adachi,M., Yamasaki,Y., Iriye,Y., Takahashi,E., Takagi,T., Nakamura,Y. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                           The large-scale mapping of rat microsatellite markers Unpublished (1998)
2 (bases 1 to 378)
Watanabe, T. K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rattus norvegicus DNA, clone:OT33.09/752e04.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             378 bp DNA STS RATTUS NOTVEGICUS, OTSUKA Clone, OT33.09/752e04, sequence, sequence tagged site.
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Submitted (24-JUL-1998) to the DDBJ/EMBL/GenBank databas
K Watanabe, Otsuka Pharmaceutical Co., Ltd., Otsuka GEN
Institute; 463-10, Kagasuno, Kawauchi-cho, Tokushima, To
771-0192, Japan (E-mail:watanabe@otsuka.genome.ad.jp,
Tel:81-886-65-2888, Fax:81-886-37-1035)
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                                                                                                                                                             /Organism="Rattus norvegicus"
/db_xref="taxon:10116"
/db_xref="taxon:10116"
/clone="0T33.09/752e04"
/note="0T33.09/752e04"
0T33.09/752e04R=5'-AATCTTTGGTCTTTAAACCCTGC-3'"
104 c 76 g 77 t 1 others
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/db_xref="taxon:10116"
/clone="0729.32/731c19"
/clone="0729.32/731c09F=5'-GATTAGGGGACAAGGGGCT-3',
/note="0729.32/731c09F=5'-TCTGATATTCATACATGGGCTGC-3'"
0729.32/731c09R=5'-TCTGATATTCATACATGGGCTGC-3'"
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                                                 Score 37.6; DB
Pred. No. 0.61;
33; Mismatches
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Pred. No. 0.0039;
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1 (bases 1 to 7218)

Dorner, F., Scheiflinger, F. and Falkner. Recombinant fowlpox virus

Patent: US 5670367-A 14 23-SEP-1997;

Location/Qualifiers

1 7218

1 7218
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 113440)
DOE Joint Genome Institute.
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                                                                                                                               HTG; HTGS_PHASE1;
                                                                                                                                                                        Homo sapiens chromosome
SEQUENCE, 14 unordered p
AC020935
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Llarity 4.5%; Pred. No. 0.71;
Conservative 156; Mismatches
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09-FEB-2000 WORKING DRAFT

Mammalia;

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Length Indels

368 others

28-DEC-1997

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-----Summary Statistics
Consensus quality: 99051 bases at least Q30
Consensus quality: 106221 bases at least Q30
Consensus quality: 108903 bases at least Q20
Consensus quality: 108903 bases at least Q20
Estimated insert size: 113400; sum-of-contigs estimation
Estimated insert size: 115000; pulse field gel estimation
Quality coverage: 6.27x in Q20 bases; pulse field gel estimation
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2 (bases 1 to 113440)
DOE Joint Genome Institute.
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1 (bases 1 to 70480)

Sulston, J.E. and Waterston, R.

Toward a complete human genome sequence genome Res. 8 (11), 1097-1108 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC006973.2 GI:4699968 HTG.
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                                                                                                                                                                                                                                                                                                                                                                                                 Glossip,D., Bauer,C., Ames,M. The sequence of Homo sapiens I
                                                                                                                                                                                                                                                                                                                                                  3 (bases 1 to 70480) Waterston, R.H.
                                                                                                 Submitted (21-DEC-1999) Department of Genetics, University, 4444 Forest Park Avenue, St. Louis, on Apr 28, 1999 this sequence version replaced conter
                                                                                                                                                                                           Direct Submission Submitted (28-APR-1999) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA (bases 1 to 70480)
                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
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Center: Washington University Genome Sequencing Center Center code: WUGSC
Web Site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
Center project name: H_DJ0909F12
                                                                                                                                                                  Submission
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RP5-909F12 from 7q34-q36,
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s, Missouri 63108, U
d gi:4337282.
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping sequencing collaboration between the NHGRI Chromosome 7 Mapping sequencing ceren, Director), John D. McPherson in the project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information University Genome Sequencing Center. For additional information about the map position of this sequence, see about the map position of this sequence, see

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The clone sequenced to the left is RP5-1161G23, 200 bp overlap.
Actual start of this clone is at base position 83123 of
RP5-1161G23; actual end is at 70480 of RP5-909F12.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This clone was derived from human PAC library RPCI-5, prepared by Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu) using the method described by loannou et al., Nature Genetics 6:84-9 (1994). The library is from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mailto:egreen@nhgri.nih.gov , or see http://genome.wustl.edu/gsc
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/chromosome="7"
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/clone="RP5-909F12"
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35664. .39
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32447. .3
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32857. .:
                                                                                                                                                             37633. .37923
/rpt_family="Alu"
38667. .38754
                                                                                                                                                                                                                       /rpt_family="L2" 37474. .37553
                                                                                                                                                                                          /rpt_family="L2"
37633. .37923
                                                                                                                                                                                                                                                                                                                                                                                                /rpt_family="MIR" 32715. .32761
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="MER1_type" 23848. .23967
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19578. .19893
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19179. .19458
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0567. .20627
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                                                                                                11.8%; Score 37; DB 39; Length 70480; 28.2%; Pred. No. 1.2; tive 31; Mismatches 30; Indels 0
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L. .24745
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                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 173618)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HTG 13-MAR-2000 Homo sapiens chromosome UL clone RP11-63G23, WORKING DRAFT SEQUENCE, 18 unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      양점
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (30-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Center: Washington University Genome Sequencing Center Center code: WUGSC
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Waterston, R.H.
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                                                                                                                                                                                                                                                                                                                                                                                                    Quality coverage: 3.64 in Q20 bases; agarose-fp Quality coverage: 4.09 in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Web site:http://genome.wustl.edu/gsc/index.shtml
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence of Homo sapiens clone
                                                                                                                                                                                                                                                               NOTE: This is a 'working draft' sequence. It currently consists of 18 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
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                                                                                                                                                                                                                                                                                                                                                                                                                           Mouse enzyme
M88481
                                                                                                                                                                                        2 (bases 1 to 2041)
Tucker, P.K., Phillips, K.S. and Lundrigan, B
A mouse Y chromosome pseudogene is related
                                                                                                                                                                                                                                                                                                                Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; 1 (bases 1 to 2041)
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Eutheria: Rodentia; Sciuroqnathi; Muridae; Murinae; Mus
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Mus musculus (strain 163H) male DNA.
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Location/Qualifiers
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30229 c 30623 g 53714 t
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/db_xref="taxon:9606"
/chromosome="UL"
                         join(372. .443,680. .877,1438. .1512,1617.
/gene="E1"
372. .443"
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                                                                                       /organism="Mus musculus"
/strain="163H"
/db_xref="taxon:10090"
/note="putative"
                                                                          /sex="male"
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83830: contig of 10077 bp in length
83930: gap of unknown length
83930: gap of unknown length
99489: contig of 15459 bp in length
13715: contig of 14226 bp in length
13915: gap of unknown length
139051: contig of 25236 bp in length
139151: gap of unknown length
           'gene="E1"
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E1 (E1)
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Gaps

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                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 16832)
Adams, M. and Veneer, J.C.
                                                                                                                                                              Submitted (16-NOV-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10211489 by the submitte For further information on this sequence e-mail to fly@celer* NOTE: This is a 'working draft' sequence.
                                                                                                                                                                                                                                                                                                                                                           AC014255.1 GI:6437080
HTG: HTGS_PHASE2.
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Drosophila melanogaster,
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                                                                                                                  This sequence will be replaced by the finished sequence as soon as it is available and the accession number will be preserved.
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                                                   /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
3392 c 3347 g 5089 t
                                                                                                                 Location/Qualifiers
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/note-"
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463 c
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/citation=[2]
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/citation=[2]
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/citation=[2]
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∕gene="E1"
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%; Pred. No. 1.8;
33; Mismatches
   Score 36;
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to fly@celera.com.
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RS Muzny,D.M., Adams,C., Bailey,M., Barbaria,J., Blankenburg,K., Bodota,B., Bouck,J., Bowie,S., Brooks,A., Buhay,C., Bunac,C., Burkett,C., Burows,J., Carter,M., Chacko,J., Chen,Z., Cox,C., David,R., Delgado,O., Deshazo,D., Ding,Y., Domah-Rashid,N., Frantz,P., Ganesh,R., Gorrell,J.H., Gorrell,L.L., Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Holloway,C., Hosak,H., Jackson,L.E., Jackson,L., Jia,Y., Jones,M., Kelly,S., Kondejewski,N., Kong,Y., Kovar,C., Leal,B., Li,Z., Martin,R., Martinez,C., McLeod,M.P., Mei,G., Morgan,M., Morris,S., Nash,S., Nelson,A., Nguyen,R., Nguyen,N., Nguyen,S., Oswal,G., Parish,B., Paxton,S., Payton,B., Perez,L., Pu,L.L., Oulles,M., Shen,H., Simon,M., Samuel,S., Say,J., Scherer,S., Shah,E., Taylor,T., Vasquez,L., Vinson,R., Worley,R., Watlington,S., Weinstock,G., Weinstock,I.R., Williamson,A., Worley,K., Watlington,S., Direct Submission

CE (bases 1 to 88866)
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (18-SEP-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Sep 22, 1999 this sequence version replaced gi:5902995.

NOTE: This is a 'working draft' sequence. It currently consists of 69 contigs. The true order of the pieces is not known and their order in this sequence record is a rithrary. Gaps between the contigs are represented as arbitrary. Gaps between the contigs are unknown.

* This record will be updated with the finished sequence
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Direct Submission
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Drosophila melanogaster
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Drosophila melanogaster clone RPC198-154F9,
PROGRESS ***, 69 unordered pieces.
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852: contig of 852 bp in length 163: contig of 831 bp in length 2542: contig of 859 bp in length 3916: contig of 859 bp in length 648: contig of 1374 bp in length 7285: contig of 1312 bp in length 8163: contig of 878 bp in length 9100: contig of 878 bp in length 10441: contig of 978 bp in length 11652: contig of 1341 bp in length 12386: contig of 137 bp in length 10491; contig of 137 bp in length 10491; contig of 1310 bp in length 12386: contig of 1311 bp in length
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8; Mismatches
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Blazej, R.G.,

Karra, K.,

Insecta;

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                                                                                                  Conservative
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/db_xref="taxon:7227"
/clone="RPCI98-154F9"
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1. .88866
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                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Submitted (02-AUG-1999) Drosophila Genome Center, Lawrence Berkeley Laboratory, MS 64-121, Berkeley, CA 94720, USA On Feb 15, 2000 this sequence version replaced gi:6435852. On Feb 15, 2000 this sequence version replaced gi:6435852. On Feb 15, 2000 this sequence, including its location For further information about this sequence, including its location For further information about this sequence, or send email archive Web site (http://www.fruitfly.pease visit our sequence to bdggefruitfly.berkeley.edu. All contigs in this submission meet the following cutoffs: length >= 200 bases.

* NOTE: This is a 'working draft' sequence. It currently * NOTE: This is a 'working draft' sequence. It currently * NOTE: This is a 'working draft' sequence record is * is not known and their order in this sequence record is * arbitrary. Gaps between the contigs are represented as * arbitrary. Gaps between the contigs are represented as * arbitrary. Gaps between the contigs are represented as * arbitrary. Gaps between the finished sequence * This record will be updated with the finished sequence * This record will be updated with the finished sequence
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Drosophila melanogaster chromosome 3 clone BACR43K14 (D968) RPCI-98
43.K.14 map 85D-85D strain y; cn bw sp, *** SEQUENCING IN PROGRESS
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Butenhoff, C., Champe, M., Chavez, C., Chew, M., Ciesiolka, L.,
Doyle, C.M., Farfan, D.E., Galle, R., George, R.A., Harris, N.L.,
Hinkle, A., Hoskins, R.A., Houston, K.A., Hummasti, S.R., Karra, F
Kaarney, L., Lee, B., Lewis, S., Lip, Ling, H., Moshrefi, A.R.,
Moshrefi, M., Nixon, Pacleb, J.M., Park, S., Pfeiffer, B.,
Richards, S., Sethi, H., Svirskas, R.R., Wan, K.H., Webster, D.,
Woolley, P., Yang, S., Yee, M., Yu, C. and Rubin, G.M.
Sequencing of Drosophila melanogaster
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 114958)
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be preserved.
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24344 25054 25054 267024 31946 32925 32929 33009 35166 32929 35166 36534 36634

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Search completed: August 7, 2000, 10:55:16 Job time: 6090 sec

Db 57676 TTTGTTTGCTGCCTTTTGTTCGCTTGTAGTGG 57645

Sequence Patent No. Sequence

Appli

Sequence

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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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US-09-226-568-18
US-09-211-640-1
US-09-211-640-1
US-08-08-945A-1
US-08-08-945A-1
US-08-22-177A-52
US-08-162-081B-34
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                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.
APPLICATION NOTA:
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US-08-232-463-14
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PATENT NO. 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: SCHEIFLINGER, F.
APPLICANT: FALKNER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
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                              LENGTH: 7218 base pair
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: pTZgpt-F1s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSE: Foley & Lardner
STREET: 1800 Diagonal Road,
CITY: Alexandria
STATE: VA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
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US-08-484-158B-9
US-08-480-150A-9
US-08-489-131-9
US-08-458-731-9
US-08-146-930-3
US-08-146-930-3
PCT-US93-0399-3
US-08-716-679-2
US-08-716-679-2
US-08-71-6498-13
US-07-989-947-11
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                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: OKADA, YUKIO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: 1TO, KAZUTOSHI
APPLICANT: KIHARA, MAKOTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 1, Application US/08793599 Patent No. 5952489
                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER FILE REFERENCE: 2589-0056-0 PCT CURRENT APPLICATION NUMBER: US/08/793,599 CURRENT FILING DATE: 1997-03-04 PERILIER APPLICATION NUMBER: PCT/JF96/01866 EARLIER FILING DATE: 1996-07-05 EARLIER APPLICATION NUMBER: JP 191028/1995 EARLIER FILING DATE: 1995-07-05
GENERAL INFORMATION:
APPLICANT: OKADA, YUKIO
APPLICANT: YOSHIGI, NAOHIRO
APPLICANT: ITO, KAZUTOSHI
                                                         sequence 3, Application US/08793599 Patent No. 5952489
                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn
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                                                                                                                                                                              164
                                                                                                                                                                                                                                                                 Match 9.7%; Score 30.6; DB 4;
Local Similarity 27.1%; Pred. No. 0.67;
Nes 23; Conservative 28; Mismatches 34;
                                                                                                                                                  76
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                                                                                                                                                 GTTTCCTTAATTTATTTCATGCCTT
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CURRENT APPLICATION NUMBER: US/09/226,568
CURRENT FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 18
LENGTH: 3934
TYPE: DNA
ORGANISM: Homo sapiens
FEBTURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TYPE: DNA
; ORGANISM: Barley
US-08-793-599-3
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                                                                                                                                                                                                                                                                              ; OTHER INFORMATION: Description of Artificial Sequence: antisense ; OTHER INFORMATION: sequence US-09-226-568-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER FILING DATE: 1995-07-05
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 3
LENGTH: 2142
                                                                          US-08-077-848A-1/c
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                                                                                           RESULT
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TITLE OF INVENTION: TISSUE-SPECIFIC PROMOTER
FILE REFERENCE: 2589-0056-0 PCT
CURRENT APPLICATION NUMBER: US/08/793,599
CURRENT FILING DATE: 1997-03-04
EARLIER APPLICATION NUMBER: PCT/JP96/01866
EARLIER FILING DATE: 1996-07-05
EARLIER APPLICATION NUMBER: JP 191028/1995
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: ACKERMANN, Elizabeth J.
APPLICANT: Bennett, C. Frank
APPLICANT: Bean, Nicholas M.
APPLICANT: Marcusson, Eric G.
APPLICANT: Marcusson, Eric G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence 18, Application US/09226568
patent No. 6001992
                                           Sequence 1, Application Patent No. 5470955
                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                  Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Antisense modulation of TITLE OF INVENTION: bcl-2-Related Proteins FILE REFERENCE: ISPH-0337
              GENERAL INFORMATION:
APPLICANT: Craig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    164 gunaccungugunuguncgucacun 188
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                                                                                                                                         600
                                                                                                                                                       261 cuccagugucuuccguuuguacucguccuccuccuccuccuccuccucggccgg 308
                                                                                                                                        23;
                                                                                                                                                                                                       al Similarity
27; Conserv
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                                                               US/08077848A
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                                                                                                                                                                                                          9;
                                                                                                                                                                                                          Score 28.8; DF
Pred. No. 4.3;
9; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 30.6; DB Pred. No. 0.84;
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      SPECIFICALLY BIND mcl-1
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STREET: 1000 CITY: LOS Angeles CTATE: California

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equence 1, Application US/09211640
Atent No. 6020466
                                                                                                                    COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARATTERISTICS:
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NAME: Halle, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ANDRESCER: CARRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE: Californ.
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
ATTORNEY TOWNS ATTORNEY TOWNS ATTORNEY TO THE PARTY OF THE P
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 3946 base pairs
TYPE: nucleic acid
                                                    PatentIn Release #1.0, Version #1.25
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E: DNA (genomic)
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amino acid 227 = A; when nucleotide 740 = T, amino
acid 227 = v."
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     COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: PCT/US94/03547
FILING DATE: 31-MAR-1994
CLASSIFICATION:
NAME: Wetherell, Jr., Ph.D., John W.
REGISTRATION NUMBER: BD-2845
REFERENCE/DOCKET NUMBER: BD-2845
TELEOPHONE: (619) 455-5110
TIBLEPAX: (619) 455-5110
TIBLEPAX: (619) 455-5110
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Best Local Similarity 50...
"Anhes 27; Conservative
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application GENERAL INFORMATION APPLICANT: The Journal of the Journal
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TELEPHONE: (619) 455-5100
TELEPAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: The Johns Hopkins University School of Medicine TITLE OF INVENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE TITLE OF INVENTION: MCL-1
NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: US
ZIP: 90067
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TOPOLOGY: linea
MOLECULE TYPE: DN
IMMEDIATE SOURCE:
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LOCATION: 61..1110
OTHER INFORMATION: OTHER INFORMATION: COTHER INFORMAT
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NAME: Haile, Ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: PD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Spensley Horn Jubas & Lubitz STREET: 1880 Century Park East, Suite 500 STATE: California
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APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/211,640
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLONE: mcl-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application PC/TUS9403547
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PE: DNA (genomic)
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Pred. No. 4.3;
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NAME/KEY: CDS
LOCATION: 61.1110
LOCATION: 61.1110
COTHER INFORMATION: 0
COTHER INFORMATION: 0
US-08-077-848A-1

STRANDEDNESS:
TOPOLOGY: 11n
MOLECULE TYPE:

single

IMMEDIATE SOURCE:

CLONE:

mcl-1

US-09-211-640-1/c

GENERAL INFORMATION:

APPLICANT:

COUNTRY:

USA

California

90067

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Query Match Best Local (Matches

Similarity

Conservative

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NAME/KEY: CDS
LOCATION: 61..110
COTHER INFORMATION: /
OTHER INFORMATION: a
OTHER INFORMATION: a
PCT-US94-03547-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: line:
MOLECULE TYPE: D:
IMMEDIATE SOURCE:
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                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
SOFTWARE: PatentION DATA:
CURRENT APPLICATION NUMBER: US/08/068,945A
APPLICATION NUMBER: US/08/068,945A
FILING DATE: 27-MAY-1993
FILING DATE: 27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                             APPLICATION NUMBER: SE 9201826-6
FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 5
FILING DATE: 11-JUN-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                  FILING DATE: 11-JUN-1992
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRANDEDNESS:
                                  APPLICATION NUMBER: SE 9
FILING DATE: 19-MAR-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH:
                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
NAME: Sterner, Richard J. REGISTRATION NUMBER: 35,372 REFERENCE/DOCKET NUMBER: 11
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11 Similarity 56.2%;
27; Conservative
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Nilseco
                                                                                                                                                                                                                                                                                                                                                                                                                                  : White & Case
1155 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tornell, Jan
VENTION: New DNA Sequences
EQUENCES: 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                      United States
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Enerback,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
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                                                       UMBER: SE 9300902-5
19-MAR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note= "when nucleotide 740 = C, amino acid .227 = A; when nucleotide 740 = acid .227 = V."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peter
                                                                                                                                                                                                          SE 9201809-2
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Pred. No. 4.3;
9; Mismatches
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1103326-052
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LOCATION:
US-08-068-945A-1
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INFORMATION FOR SEQ ID NO: 1:
Query Match 9.2%;
Best Local Similarity 33.6%;
Matches 51; Conservative 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
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NAME/KEY:
LOCATION:
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NAME/KEY:
LOCATION:
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
NAME/KEY:
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                                                                                                                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
TISSUE TYPE: Mammary gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                    LOCATION: FEATURE:
                                                                                                                                                                                                                  FEATURE
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                                                                                                                                         FEATURE:
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...4904, 6193..6323, 6501..6608, 6751..6868, 8335
...8521, 8719..8922, 10124..10321, 10650..11394)
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1..1640
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join(1722..1727, 4071..4221, 4307..4429, 4707)

1040(45193..6323, 6501..6608, 6751..6868, 8335)

10404, 6193..6323, 10124..10321, 10650..11391)

10521, 8719..8922, 10124..10321, 10650..11391)

RWATION: /EC_number___3.1.1.1
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4707:.4904
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4307..4429
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4071..4221
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1641..1727
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6501.
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6193.
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6751.
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8719
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8335.
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10124..10321
                                                                              3'UTR
11491..11531
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10650..11490
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                                                                                                                                                                                                                                .8521
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         score 28.8; DI
pred. No. 6.9;
24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bile Salt-Stimulated Lipase"
                                  DB 1;
                                  Length 11531;
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24;

77;

0;

Gaps

4

101

US-08-442-806-1

tent No.

Application US/08442806

INFORMATION:

Bjursell, Gunnar

Enerback,

Sven Peter

Nilsson, Jeanette

n, Lennart 9, Ulf

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7227 GGAGTTTCATCGTGTTAGCTAGGATGATCTCG 7258

161 unuguuaccunguguuuguucgucacungucg 192

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GCTCACTGCAACCTCCACCTCCTGGGTTCAAGTGATTCTCTGACTCAACCTCCCATGTAG 7166
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US-08-442-806-1
                                                                                            Query Match 9.2
Best Local Similarity 33.6
Matches 51; Conservative
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7167 CTGGGACTACAGGCACATGCCACCATGCCCAGATAATTTTTCTGTGTGTTTTAGTAGGGAT 7226
                  FEATURE:
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ORIGINAL SOURCE:
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11491..11531
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10124..10321
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8719.
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8335.
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6751
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join(1722..1727, 4071..4221, 4307..4429, 4707
..4904, 6193..6323, 6501..6608, 6751..6868, 8335
..8521, 8719..8922, 10124..10321, 10650..11391)
ORWATION: /EC_number= 3.1.1.1
ORWATION: /EC_number= 3.1.1.1
                                                                                                                                                                                               exon
10650..11490
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1611..1617
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6501.
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6193
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..4904, 6103..6323, 6501..6608, 6751..6868, 833
..8521, 8719..8922, 10124..10321, 10650..11394)
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4307..4429
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1..1640
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4071..4221
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1641..1727
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                                                                                        9.2%; Score 28.8; DB 2; 33.6%; Pred. No. 6.9; tive 24; Mismatches 77;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product= "Bile Salt-Stimulated Lipase"
                                                                                           77;
                                                                                                             Length 11531;
                                                                                         Indels
                                                                                       0,
                                                                                     Gaps
                                            7166
                                                                                      0;
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TELEFAX: (212)354-8113
NFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS:

ENGTH:

nucleic acid

REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212,819-8783

1103326-052

PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9300902-5
FILING DATE: 19-MAR-1993

FILING DATE: 19-MAR-1993 ATTORNEY/AGENT INFORMATION:

Richard

FILING DATE: 12-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9202088-2
FILING DATE: 03-JUL-1992

UMBER: SE 9201826-6 12-JUN-1992

FILING LA... 435
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9201809-2
APPLICATION NUMBER: 11-JUN-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US OF FILING DATE: 27-MAY-1993

US 08/068,945

APPLICATION NUMBER: FILING DATE: CLASSIFICATION: 435

US/08/442,806

Version

#1

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: ISM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:

COUNTRY: United States ZIP: 10036-2787

New York

CORRESPONDENCE ADDRESS:

ADDRESSEE:

SSEE: White & Case F: 1155 Avenue of the Americas New York

ITLE OF INVENTION:

Encoding Human BSSL/CEL Genomic DNA Sequences

FILING DATE: 11-JUN-:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:

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192

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US-08-222-177A-17
Sequence 17, Application US/08222177A
; Patent No. 5582979
; GENERAL INFORMATION:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341/562
APPLICATION NUMBER: US 07/341/562
APPLICATION NUMBER: US 07/341/562
APPLICATION NUMBER: US 07/341/562
APPLICATION NUMBER: 30,492
REGISTRATION NUMBER: 09865.601
REFERENCE/DOCKET NUMBER: 09865.601
TELEPHONE: (608) 831-2106
TELEPHONE: (608) 831-2106
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ZIP: 53717-1914
COMPUTER READABLE FORM:
COMPUTER FLADABLE FORM:
FLADABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,17
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                                                                                                                                                                                                                                      FEATURE:
NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 221 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: 1
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                         POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                                        IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                       OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                          TISSUE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                 OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                       CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                         INDIVIDUAL ISOLATE
                                                                                                                      IDENTIFICATION METHOD:
NAME/KEY: misc_feature
LOCATION: complement (144..163)
IDENTIFICATION METHOD: experime
                                                                                                                                                      NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
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8000 Excelsior Drive, Suite 401
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                                                                                                                                                          feature
                                                                                                                                                                                       /rpt_type= "tandem"
/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
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                                                                   /evidence= EXPERIMENTAL
/standard_name= "PCR pr:
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                  Caucasian
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                                                                                                                       experimental
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                                                                                          "PCR primer"
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RESULT 11
US-08-222-177A-52
US-08-222-177A-52
; Sequence 52, Application of the sequence 52, Application of the sequence of th
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Best Local Similarity
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IDENTIFICATION METHOD: 6
OTHER INFORMATION: /evi
OTHER INFORMATION: /stal
PUBLICATION INFORMATION:
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OTHER INFORMATION:
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                                                                                                                                                              COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222,177
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY:
CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: LENGTH POLYMORPHISMS IN (dC-dA)n. (dG-dT)n SEQUEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
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DATE: 1989
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CITY: Madison
STATE: Wiscons
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ZIP: 53717-1914
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Abundant Class of Human DNA Polymorphisms Which Can Be Typed Using the Polymerase C
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/standard_name= "PCR primer"
/citation= ([1])
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28.9%; Pred. No. 1.
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/evidence= EXPERIMENTAL
                                                                                                                                                                                                              US/08/222,177A
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                                                                                                                                                                                                                                                                                   Version #1.25
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NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 090
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100

30,492 ER: 09865.601

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US-08-222-177A-52
                            TITLE: Abundant Class of Human DNA Polymorphisms TITLE: Reaction Be Typed Using the Polymerasa TURNAL: Am. J. Hum. Genet PAGES:
                                                                                                                                                                                                                                                                                                                                                                                                                             IDENTIFICATION: complement (198..217)
IDENTIFICATION METHOD: experimental
OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /standard_name= "PCR primer"
COTHER INFORMATION: /citation= ([1])
FRATURE:
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                                                                                                                                                                                                                                                                                                                               PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURE:
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CHROMOSOME/SEGMENT:
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CLONE: Mfd154
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ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                        AUTHORS:
                                                                                                                                                                                          AUTHORS: Wasmuth, J. J.
TITLE: Mapping of human chromosome
TITLE: polymorphisms
                                                                                                                                                                                                                                                                                                                                              LOCATION: 1.278
IDENTIFICATION METHOD:
OTHER INFORMATION: /ev:
OTHER INFORMATION: /sta
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OTHER INFORMATION:
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OTHER INFORMATION:
OTHER INFORMATION:
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INDIVIDUAL ISOLATE: Cau
TISSUE TYPE: Blood
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                          388-396
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                                                                                                                                                                                                                                                                  Polymeropoulos, M. H. May, P. E. Kwitek, A. E.
                                                                                                                                                                                Genomics
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                                                                                                                                                                                                                                                        Xiao, H.
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20..39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OD: experimental voldence EXPERIMENTAL /Standard_name= "PCR primer" /citation= ([1])
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/rpt_family= "(dC-dA)n.(dG-dT)n"
/citation= ([2])
                                                                                                                                                                                                                                                                                                                                       /standard_name= "Only one strand sequenced"
                                                                                                                                                                                                                                                                                                                                                        D: experimental
/evidence= EXPERIMENTAL
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US-08-162-081B-34
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                                                                                                             Matches
                                                                                                                                       Query Match
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                                                                                                                                                                                                                                           TELEFAX: (212) 838-388
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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Best Local Similarity 30.5
Matches 32; Conservative
                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UDMER: PCT/GB93/00
FILING DATE: 13 April 1993
ATTORNEY/AGENT INFORMATION:
NAME: PASQUALINI, PATTICIA A.
REGISTRATION NUMBER: 34,894
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                              2535 GGGACTTATTGAGGTG 2550
                                                             REFERENCE/DOCKET NUMBER: LUTELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Hiles, Ian Donald; Fry, Michael John; Dhand, Ritu APPLICANT: Bala; Waterfield, Michael Derek; Parker, Peter APPLICANT: Joseph; Otsu, Masayuki; Panayotou, George; Volinia, TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY, THEIR PREPARATION AND USE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                          Local
                                                                                                                                                                                                   LENGTH: 3240 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/162,081B
FILING DATE: February 7, 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PS/
OPERATING SYSTEM:
                                                                                                                                                                                               POPOLOGY:
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                        ccugcgaauuggugug
                                                                                                            l Similarity
26; Conserv
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TD NO: 34:
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                                                                                                         Conservative
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                                                                                                    Score 28; DB 2;
Pred. No. 7.2;
0; Mismatches ?
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Pred. No. 2.1;
25; Mismatches 48;
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                                                                                                       30;
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                                                                                                                                Length 3240;
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US-08-162-081B-32
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                                                           Sequence 32, Application.

Sequence 32, Applicat
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Joseph; Otsu, masayuni, applicant: Stefano; Gout, Ivan Tarasovitch APPLICANT: Stefano; GOUT, IVAN TARAS ACTIVITY, TITLE OF INVENTION: THEIR PREPARATION AND USE TITLE OF INVENTION: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 13 APTIL 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricia A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2535 GGGACTTATTGAGGTG 2550
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OPERATING SYSTEM: PC-DOS
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TITLE OF INVENTION:
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STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          200 ccugcgaauuggugug 215
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FILING DATE: February 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 April 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Watch 8.9%; Score 28; DB 3; Local Similarity 34.2%; Pred. No. 7.2; Local Similarity 20; Mismatches 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             aagucgugguuuguuguuuguuaccuuguguuuguucgucacuugucgacagcgc 199
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805 Third Avenue
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Bala; Waterfield, Michael Derek; Parker, Peter
Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
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                                                                                                   Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
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                                            Gout, Ivan Tarasovitch
POLYPEPTIDES HAVING KINASE ACTIVITY
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; NAME/KEY: CDS
; LOCATION: 1..3204
; OTHER INFORMATION:
US-08-162-081B-32
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REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 52
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 688-9200
TELEPAX: (212) 688-9804
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
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Best Local :
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FILING DATE: February 7,
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GI
FILING DATE: 13 APril 1993
ATTORNEY/AGENT INFORMATION:
NAME: Pasqualini, Patricti
                                                                                                                                                                                                                                                                          Sequence 32, Patent No. 5
                                                                                                                                                                                                                                                          GENERAL INFORMATION:
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CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
COMPUTER: IBM PS/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                              2535 GGGACTTATTGAGGTG 2550
                                                                                                   NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Felfe & Lynch
                                                                                                                                                     APPLICANT: Joseph; Otsu, Masayuki; Panayotsu, George; Vo
APPLICANT: Stefano; Gout, Ivan Tarasovitch
TITLE OF INVENTION: POLYPEPTIDES HAVING KINASE ACTIVITY,
TITLE OF INVENTION: THEIR PREPARATION AND USE
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SOFTWARE: Wordper
COMPUTER READABLE FORM:
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les 26; Conserv
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                    COUNTRY: C
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                                                                                STREET:
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E: New York
TRY: USA
                                                                    New York
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                                                   New York
                                                                                                                                                                                                                                                                                             Application US/08780872
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Bala; Waterfield, Michael Derek; Parker, Peter
Joseph; Otsu, Masayuki; Panayotou, George; Volinia,
Stefano; Gout, Ivan Tarasovitch
                                                                                    805 Third Avenue
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                                  USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8.9%; Score 28; DB 2; 34.2%; Pred. No. 7.4;
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MEDIUM TYPE: Diskette, 5.25 inch, 360 MCCOMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,872
FILING DATE: 09-JAN-1997
CLASSIFICATION OPTAN: 435
PRIOR APPLICATION NUMBER: 08/162,081
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: FEBRUARY 7, 1994
APPLICATION NUMBER: PCT/GB93/00761
FILING DATE: 13 APT11 1993
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5256
TELEPHONE: (212) 688-9200
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 3412 base pairs
TYPE: nucleic acid
STRANDEDNESS: single or double
TOPOLOGY: Linear
                                                                                                                                                                                                                                                      NAME/KEY: CDS: LOCATION: 1.3204; OTHER INFORMATION: US-08-780-872-32
                                                                                                                                                  Query Match 8.9
Best Local Similarity 34.2
Matches 26; Conservative
2535 GGGACTTATTGAGGTG 2550
                                                             200 ccugcgaauuggugug 215
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                                                                                                                                          8.9%; Score 28; DB 3; Length 3412; 34.2%; Pred. No. 7.4; ative 20; Mismatches 30; Indels
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Search completed: August 7, 2000, 09:28:54 Job time: 908 sec

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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 7, 2000, 09:21:25; Search time 205.61 Seconds (without alignments) 382.084 Million cell updates/sec

Title: Perfect score: Sequence: US-09-214-124-2_COPY_265_578

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Scoring table: IDENTITY_NUC Gapext 1.0

Searched:

311585 seqs, 125096042 residues

Total number of hits satisfying chosen parameters: 623170

Minimum DB seq length: 0 Maximum DB seq length: 1000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_36:*

Pred. No. 1s the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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Query Match 100.0%; Score 314; DB 1; Length 578; Best Local Similarity 100.0%; Pred. No. 7.4e-91; Matches 314; Conservative 0; Mismatches 0; Indels

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gguaccucgcgaggguuugggaggaucggaguggcgggacgcugccgggaagcuccaccu 60

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325

K. pneumoniae diol Nucleotide sequenc	T47874 V27148	р р	4746 11832	8 8 6 6	27 27	4.4 5	oο	
Human epidermal su	Q45332 T95887	_	2487 2488	თ თ თ თ	27	42		
Murine interlenkin	Q47834	-	2281	8	27	4		
Carcinoembryonic a	V35773	, د	1830	8	27	40	Ω	
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ALIGNMENTS

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139 C; 1/2 G; 173 U;	recombinant polypeptides or production of transgenic animals.	vector. The vectors can be used for gene therapy production of a retroviral	in a vector for nermitating or only the relative some entry site (IRES)	5' derived common and Moloney murine leukaemia virus (MOMLV). The	of the genomic RNA of a type C retrovirus other than Friend murine	describes nucleotide sequence derived from all or narr of the sequence	Reticuloendotheliosis virus type A (REV-A) who moniforming RNA of	The present sequence is derived from the 5' and of the second sequence is defined as the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the second sequence is derived from the 5' and of the 5' an	Claim 6; Page 32: 43pp: French	derived from type C retroving other than analysis encapsidation enhancer -	Expression Vectors containing TRES and ()	WPI; 99-037487/04.	Darlix JL, Gabus Darliy C TIONS IN HELICABE.	SANTE & PECU	28-APR-1997; FR-005203.	28-APR-1997; 005203.	30-OCT-1998.	FR2762615-A1.	Reticuloendotheliosis virus.	retroviral vector; gene therapy; ss	type C retrovirus; internal ribosome entry site. The constitution	ype A:	Sequence derived from the 5' end of REV-A	17-MAR-1999 (first entry)	V63779;	V63779 standard; DNA; 578 RP.	779	11.77 1

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Best Local Sin
Matches 314;
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Requence derived from the 5' end of R
Reticuloendotheliosis virus type A; R
type C retrovirus; internal ribosome
retroviral vector; gene therapy; ss.
Reticuloendotheliosis virus.
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20-MAY-1999 (first entry)
Fowlpox virus (FPV S) 5' LTR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus; REV;
                       X26113
                              X26113
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                                                                                               UACUUUGGAGAGUCUUUUGCCCUCCAGUGUCUUCCGUUUGUACUCGUCCUCCUCCCCCC
                                                                   CCGGCCGGGAUGGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         standard;
                                                                                                                                                                                                                                                h 100.0%; Score
Similarity 100.0%; Pred.
14; Conservative 0; Mism
                              standard; DNA; 4643
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                                BP.
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A; REV-A; 5' end genomic
some entry site; IRES; enc
                                                                                                                                                                                                                                                    Mismatches
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No. 8.9e-91;
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proccurrence in chickens

Sclaim 18; Fig 6; 127pp; English.

CC The invention relates to a recombinant fowlpox virus (FPV) whose nucleic combinant fowlpox virus (REV), and caid does not encode an active reticuloendotheliosis virus (REV), and combinant fowlpox virus. The recombinant FPV is whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be prevent the occurrence of fowlpox virus in chickens. The chickens can be vaccinated at older than 1 day of age. Alternatively, chickens can be vaccinated at older than 1 day of age. Prior vaccine and field strains compared for provide the vaccine subsequent to vaccination with the vaccinated at the vaccine and field strains compared for contamination provides the means by which a FPV strains carry a contamination by REV may be produced. Sequences X26110-115 represent FPV contamination by REV may be produced. Sequences X26110-115 represent FPV contamination by REV may be produced. Sequences X26110-115 represent FPV contamination by REV may be produced. Sequences X26110-115 represent FPV contamination provides the means by which a FPV vaccine free from contamination by REV may be produced. Sequences X26110-115 represent FPV contamination by REV may be produced. Sequences X26110-115 represent FPV sequences X2612-115 and TPV nucleic acid molecule can comprise a FPV LTR sequence selected from the above.

Sequence 4643 BP; 1326 A; 1015 C; 1127 G; 1175 T;
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Q76041
Q76041
ID
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PD 2
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Best Local S
Matches 215
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W09907852-Al.
18-FEB-1999, AU0628.
07-AUG-1998, AU-008454.
08-AUG-1997, AU-008454.
COMMONWEALTH SCI & IND RES
                                                                                                                                                        Q76041 standard; DNA; 3878 BP
Q76041;
20-JUL-1995 (first entry)
Retrovirus vector pP0115-R1
Retrovirus; vector; pP0115-R1
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Boyle DB, Coupar BEH, Gould
WPI; 99-167428/14
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Recombinant vaccine against fowlpox virus - is free of contamination from refront vaccine against fowlpox virus - is free of contamination from refront re
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spleen necrosis virus.
w09429437-A.
22-nec-10-1
  22-DEC-1994;
07-JUN-1994;
07-JUN-1993;
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nes 215; Conserv
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                                                                                                                                                                         spleen necrosis virus;
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L.9e-87;
nes 6;
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07-JUN-1994; U06415.
07-JUN-1993; US-073345.
(UYNE-) UNIV WHO JERSEY.
DOINDUIG RC:
WPI; 95-036467/05.
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Best Local Similarity
Matches 198; Conserv
Recombinant retrovirus vector, contg. non-retroviral gene, - hability to produce progeny virus, in helper cell which can inf host cell and form provirus
Example; Page 16-17; 28pp; English.
New recombination-free, highly efficient retroviral vectors pPol11-R1 (given in Q76038), pPol11-R2 (Q76039) and pPol11-R3 (Q76040) were obtained by replacing the U3 region of the left and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-0UL-1995 (first entry)
20-UUL-1995 (first entry)
Retrovirus vector pPO111-R3; spleen necrosis virus;
Retrovirus; vector; pPO111-R3; spleen necrosis virus;
Cytomegalovirus; CMV; intermediate-early promoter; IE
Cytomegalovirus; CMV; intermediate-early promoter; IE
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Example; Page 17; 28pp; English.
The universal retroviral vector pPO115-R1 (given in 076041) was obtained by replacing the SV40 promoter and hpt gene of pPO111-R1 (076038) with the multiple cloning site of pBluescript II KS. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T;
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Spleen necrosis virus.
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Example: Page 13-14; 28pp; English.

Example: Page 13-14; 28pp; English.

Rew recombination-free, highly efficient retroviral vectors new recombination of the poilt-R3 pp0111-R1 (given in 076038), pp0111-R2 (076039) and pp0111-R3 (076040) were obtained by replacing the U3 region of the left (076040) were obtained by replacing the U3 region of the left LTR of spleen necrosis virus with the IE promoter/enhancer of CMV and extension of the encapsidation region. The vectors allow cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5528 BP; 1265 A; 1423 C; 1457 G; 1383 T;
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gcggcuugcgaauaauacuuuggagagucuuuugccuccagugucuuccguuuguacucg
                                                                            uaccuuguguuuguucgucacuugucgacagcgcccugcgaauuggugugcccacaccgc
                                                                                                                                         CCTCCGCTCAGCAGGGGGACGCCCTGACCTGAGCTCGAATTCAGATCTTGTGGTATCTGAT 1084
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nilarity 64.0%;
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Pred. No. 1.8e
96; Mismatches
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ranti-Saureus vaccines

PS Claim 1; Page 1025-1028; 3271pp; English.

PS Claim 1; Page 1025-1028; 3271pp; English.

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences

CC This sequence represents one of 5191 Staphylococcus aureus DNA sequences

CC medium, preferably selected from a floppy or hard disk, random access

CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

CC memory (RAM), read-only memory (ROM) or CD-ROM. Homology searches using

CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC that protein-encoding or regulatory regions of commercial, therapeutic or

CC industrial importance can be obtained. Specifically, sequences which are

CC includity to encode antigens have been identified and these polypeptides can

CC saureus in a vaccine composition against s.aureus infection of

CC saureus in a sample. S.aureus is implicated in numerous human diseases,

CC including cellulitis, eyelid infections, food poisoning, osteomyelitis,

CC including cellulitis, eyelid infections, scalded skin syndrome, toxic shock

CC syndrome, etc. Organisms transformed with the DNA sequences can be used

CC computer readable medium.

CC computer readable medium.

CC computer readable medium.

3377 A; 990 C; 641 G; 1808 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Staphylococcus aureus contig SEQ ID #241.

Computer readable medium; vaccine; S.aureus infection; immunc cellulitis; eyelid infection; food poisoning; osteomyelitis; cellulitis; eyelid infection; food poisoning; osteomyelitis; skin infection; surgical wound infection; scalded skin syndrously infection;
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07-JAN-1997;
05-JAN-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                       07-JAN-1997; 100117.
05-JAN-1996; US-009861.
(HUMA-) HUMAN GENOME SCI INC.
Barash SC, Choi GH, Dillon PJ, Fannon MR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen
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withese bases represent a line of missing text in
the sequence listing in the specification. They
are included to maintain the nucleotide numbering
given in the specification for this DNA sequence
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Query Match Best Local

Similarity

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RESULT
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05-JUL-1995; JP-191028.
(SAPB) SAAPOOD BREWEEZES.
Ito K, Kihara M, Okada Y,
WPI: 97-108966/10.
 Expression promoter for genes inserted into plant seeds - e.g. heat-resistant beta-amylase gene inserted into barley seeds heat-resistant beta-amylase gene inserted into barley seeds Example 6; Page 20-21; 33pp; Japanese.
T62572 is a DNA molecule comprising a heat resistant promoter derived from a barley beta-amylase (EC 3.2.1.2) gene and other sequences used for integration of this promoter into a reporter plasmid. The plasmid is used for the production of transgenic barley plants
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W09702353-A1.
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T62572;
27-OCT-1997 (first er
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t Local Similarity
ches 23; Conserv:
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05-JUL-1995; JP-191028
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Barley; heat resistant; promoter; genetic engineering; transgenic;
plant; improved maturation; ds.
Hordeum vulgare.
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| GTTTCCTTAATTTATTTCATGCCTT 52
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PR 30-JUL-1997; US-054214
PR 30-JUL-1997; US-054215
PR 30-JUL-1997; US-054218
PR 30-JUL-1997; US-054218
PR 30-JUL-1997; US-054234
PR 30-JUL-1997; US-054234
PR 30-JUL-1997; US-054236
PR 18-AUG-1997; US-055968
PR 18-AUG-1997; US-055968
PR 18-AUG-1997; US-055972
PR 19-AUG-1997; US-056524
PR 19-AUG-1997; US-056524
PR 19-AUG-1997; US-056524
PR 19-AUG-1997; US-056524
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PR 19-AUG-1997; US
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Best Local S
Matches 23
disorders, immune diseases, inflammation or blood disorders.
Claim 1; Page 236-237; 312pp; English.
This sequence represents a nucleic acid molecule which encodes a secreted human protein. The gene number is given in the descriptor line. The gene immunoglobulin Fc portion (e.g. x20403) for increasing the stability of the fused protein as compared to the human protein only.
The invention relates to 83 novel genes and their fragments (nucleic acid sequences: x20412-x2049); amino acid sequences v00258-v00377) which
                                                                                                                                                                                                                                                                                                                                         New isolated human useful for diagnosi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
W09906423-A1.
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Human; secreted
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"^^12.
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                                                                                                                                                                                                                                                                    olated human genes and the secreted polypeptides they encode for diagnosis and treatment of e.g. cancers, neurological ers, immune diseases, inflammation or blood disorders
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e PA, Rosen CA, Ruben
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2142
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BP; 651
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en SM, Shi Y, Wei
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Pred. No. 2.1;
28; Mismatches
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ei Y,
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RESULT 12
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RESULT
T33007
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Matches 27
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                                                                                                                                                                                                                                                                                                                                            W094222
22-DEC-1994.
31-MAR-1994; U03547.
31-MAR-1993; US-077848.
16-JUN-1993; US-077848.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human mcl-1 g
Myeloid cell
therapeutic;
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                                                                                                                                                                                                                   develop prods. for detection and treatment of cell proliferative disorders, partic. myeloid cell leukaemia Disclosure; Page 46-49; 67pp; English. Disclosure; Page 46-49; 67pp; English. DNA encoding new myeloid cell leukemia associated gene mcl-1 was isolated from a CDNA library prepd. from ML-1 human myeloblastic isolated from a CDNA library prepd. The predicted gene product leukemia cells induced with TPA. The predicted gene product (given in R68814) contained 350 amino acids and had a mol.wt. of
                                                                                                                                                                                                                                                                                                                                   (UYJO ) UNIV
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                                                                                                                                                                                                37.3 kDa.
Sequence
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New myeloid cell leukaemia associated gene mcl-1 - used to New myeloid cell leukaemia associated gene mcl-1 - used to level myeloid cell proliferative
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            T33007 standard; DNA; 1026
T33007;
23-OCT-1996 (first entry)
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  SRY-related
                                                                                                                                         Similarity
27; Conserv
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nilarity 56.2%;
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Pred.
                                                                                                                                        Score 28.8; Pred. No. 9.9; Mismatches
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18-JUN-1996;
30-NOV-1994; 319525.
30-NOV-1994; JP-319525.
(KACH-) KACHIKU JUSEIRAN I
WPI; 96-336575/34.
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Key
cds
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Claim 1; Page 10-14; 21pp; Japanese.
This is the nucleotide sequence of a gene encoding a mouse SRY-related This is the nucleotide sequence of a gene encoding a protein. The gene was isolated from a mouse genomic library using a protein. The gene was isolated the primers 733009-10 as a probe. The screen isolated 4 Ecori fragments of 2.3, 2.8, 3.5 and 1.5 kb covering the gen isolated 4 Ecori fragments of 2.3, 2.8 ys. as genence between bases sequence analysis revealed a 240 bp HMG box sequence resulted in 7154-7393. Similarity with the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated to amplify the human SRY HMG box sequence for primers being generated generated generated generated generated generated generated generated generated gen
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Bovine and mouse
of unborn animals
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Q54222;
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                                                                                                                                                                                                                                                                  BSSL; biologically functional bile salt stimulated lipase; CEL; carboxyl ester lipase; hybridisation; milk protein; transgenic; infant milk substitute; oral; specific; lipolysis; vitamin; bill lipid malabsorbtion; cystic fibrosis; chronic pancreatitis;
                                                                                                                                                                                                                                                                                                                                        27-JUN-1994 (BSSL/CEL Gene
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DR WPI; 94-007527/01.

DR P-PSDB; R45189.

PT DNA encoding bile salt-stimulated lipase/carboxyl ester lipase -
PT substitute, contains intron sequences

SC Claim 1; Page 43-51, 76pp; English.

CC The primers (054223-28) are used to amplify fragments of the
PS CLaim 1; Page 43-51, 76pp; English.

CC The primers (054223-28) are used to amplify fragments of the
CC The primers (054223). Which encodes a bile salt-stimulated
CC ELSSL / CEL gene, (054222). Which encodes a bile salt-stimulated
CC clipase / carboxyl ester lipase which when expressed by transgenic
CC copass through the stomach and is activated in the small intestine.
CC digestion of most dietary lipids.

SQ Sequence 11531 BP; 2464 A; 3527 C; 3280 G; 2260 T;
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Best Local s
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x32297 standard; DNA; 4795 BP.
x32297;
22-JUN-1999 (first entry)
M. grisea PTH12 gene sequence.
Fungal pathogenicity; imidazole glycerol phosphate dehydratase;
carnitine acetyl transferase; membrane associated pathogenicity
homeodomain transcription factor; PTH3; PTH11; PTH12; ss.
Magnaporthe grisea.
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23-DEC-1993.
09-JUN-1993; SE0515.
11-JUN-1992; SE-001809.
12-JUN-1992; SE-001826.
03-JUL-1992; SE-002088.
19-MAR-1993; SE-00208.
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Bjursell KG, Carlsson PNI, Enerback CSM, Hansson Signature (IFP Nilsson JA, Tornell JBF, Toernell JBF;
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PF 08-SEP-1998; U18730.

PR 10-SEP-1997; U5-058460.

PA (DUPO) DU PONT DE NEMOURS & CO E I.

Sweigard JA;

PI Sweigard JA;

PR WPI; 99-229247/19.

PR P-PSDB; 706786.

PT New isolated fungal pathogenicity genes

CC The invention relates to new isolated fungal pathogenicity genes.

CC The invention relates to new isolated fungal pathogenicity genes.

CC grisea. These novel genes encode proteins (706783-86) that are highly commologous to the fungal carnitine acetyl transferase enzyme, fungal casciated pathogenicity protein or fungal nembrane comparts are pathogenicity. The novel genes are implicated in fungal casciated pathogenicity. The novel genes are implicated in fungal created fungus. The isolated genes are useful in the design of screens to sequence represents the PTH12 gene sequence.

Sequence represents the PTH12 gene sequence.

Sequence 4795 BP; 1220 A; 1338 C; 1067 G; 1170 T;
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Best Local :
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Copyright (c) 1993 - 2000 Compugen Ltd.
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A0785991 HS_3082_B
A078591 HS_5232_A
AV025668 AV025658
A20025658 AV025658
A20025658 AV025659
A3305899 zs7176897
AA305899 zs7176897
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AA321857 H40b04 x
H80010 ys65e11.s1
AA291667 zt37c12.s
AA883427 am25a12.s
T68051 yc39h11.r1
AA990158 om13e03.s
AL044713 bKFZp434F
AA748449 ny01d10.s
AA28745929 zs80b04.s
AA805967 oc20c09.s
AA463733 aaa77903.s
AA463733 aaa79903.s
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AA463733 aaa79903.s
AA463733 aaa79903.s
AA463739 ca609905.s
AA977145 y446602.r1
AA83685 oc61e11.s
AA83765789 UI-HF-BN0
AA749362 nx99940.s
AA1808383 wf94c02.x
AA1808383 wf94c02.x
AA1808383 wf94c02.x
AA1803151 oc44f10.s
AA1905146 xn66e08.s
AA1400614 t949f07.x
AA1400614 t949f07.x
AA1837707 c2828405.s
AA1476918 ca74e07.s
AA837701 zs53904.s
AA3918504 c177e01.s
AA3918504 c177e01.s
AA3740884 nz03h10.s
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B19095 T12K17-Sp6
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1 (bases 1 to 520)
1 (bases 1 to 520)
2 (donzalez Rey, E., Remisz, E., Delgado Garcia, A. and (Scharacterization of ESTs from Trypanosoma cruzi epi Unpublished (1998)
2 (dontact: Delgado Alberto Conteact: Delgado Alberto Departamento de Biologia Molecular, Lab 303 Instituto de Parasitologia y Biomedicina Consejo Superior de Investigaciones Cientificas C/11, E-18001, Granada, Spain Tel: 34 958 805058
Fax: 34 958 805058
Fax: 34 958 go3323
Seq primer: T7
High quality sequence stop: 520.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Trypanosoma cruzi
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;
Trypanosoma; Schizotrypanum.
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AI664738.1
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T12K17-Sp6 TAMU Arabidopsis
genomic survey sequence.
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                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embry Magnoliophyra; eudicotyledons; Brassicaceae; Arabidopsis.

1 (bases 1 to 646)
1 (pases 1, Dewar, K., Buehler, E., Eng, J., Dewar, K., Buehler, E.,
                                                                                                                                                                                                                                                                                                                                                                                           thale cress.
Arabidopsis thaliana
Ecker, J.

BAC End Sequences at ATGC
Unpublished (1997)
Contact: Ecker J.
Arabidopsis Thaliana Genome Center
University of Pennsylvania
Dept. of Biology, University of Per
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/strain="C1 - Brenner"
/strain="C1 - Brenner"
/db_xref="+caxon:5693"
/clone=1in114.r"
/clone="n1114.r"
/clone="mid="r". Cruzi epimastigote normalised cDNA Library
/clone="sib="1". Ecori; Site_2: NotI; cDNA library
/note="Site_1: Ecori; Site_2: NotI; cD
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dons; Rosidae; eurosids II;
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                     of Pennsylvania,
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cruzi epimastigotes
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Brassicales;
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Best Local Similarity 37.8
Matches 42; Conservative
                                     source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This clone is available royalty-free through LLNL; contact the MAGE Consortium (info@image.llnl.gov) for further information. Possible reversed clone: sinilarity on wrong strand insert Length: 2216 Std Error: 0.00 Seq primer: -41m13 fwd. ET from Amersham High quality sequence stop: 223.
                                                                                                                                                                                             Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                       Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. I
                                                                                                                                                                                                                                                           Generation and analysis of 280,000 human expressed sequence tags
Genome Res. 6 (9), 807-828 (1996)
97044478
On Sep 29, 1997 this sequence version replaced gi:1520551.
                                                                                                                                                                                                                                                                                                                                               Hillier, L. Lennon, G., Becker, M., Bonaldo, M.F., Chiapelli, B., Chispes, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutherla; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA283692 296 bp mRNA EST 08-AUG-1997 2t18b01.s1 Soares ovary tumor NDHOT Homo sapiens cDNA clone LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL1.;, mRNA seminance AA283692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
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Class: BAC ends
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .ass: BAC ends
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quality sequence stop: {
    Location/Qualifiers
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/organism="Homo sapiens'
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /sex="hermaphrodite"
/note="Vector: BeloBACII; Site_1: HindIII; Site_2:
HindIII; Produced by Rod Wing"
313 c 110 g 155 t 31 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Arabidopsis thaliana"
/strain="Columbia"
/db_xref="taxon:3702"
/clone="T12K17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib-"TAMU"
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Pred. No. 7.6;
B; Mismatches 51;
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                                                                                                                                                                                                                     Louis, MO 63108
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AI963668/c
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Best Local
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                                                                                                                                                        Email: Robert_Strausberg@nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.
Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Washington University Genome Sequencing by: Washington University Genome Sequencing that I.M.A.G.E. Consortium/LLNL at:
Insert Length: 1053 Std Error: 0.00
High quality sequence stop: 247.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tumor Gene Index
Unpublished (1997)
On Jul 27, 1999 this sequence version replaced gi:4059330
Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Fmail: Robert 51550
                                                                                                                                                                                                                                                                                                                                                                                                                       NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; 1
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1_(bases 1 to 259)
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wr64e02.x1 NCI_CGAP_Ut1
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27; Conserv
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                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
/dlone="IMAGE:2492474"
/clone_lib="NCI_CGAP_Utl"
/tissue_type="well-differentiated endometrial
                                                                    adenocarcinoma,
/note="Organ: uterus; vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. primer: Oligo dT.
Average insert size 1.75 kb. Life Technologies catalog #:
                                             /lab_host="DH10B"
/note="no---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:713449"
/clone_lib="Soares ovary tumor NbHOT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contains element MSR1
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Pred. No. 12;
10; Mismatches
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Homo sapiens cDNA clone IMAGE:2492474
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HS_3082_B2_D02_MR CIT Approved Human Genomic Sperm Library D
Homo sapiens genomic clone Plate=3082 Col=4 Row=H, genomic
survey_sequence.
                                                                                                                                                                                                                                                                                401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-387
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3082 row: H column: 4
Seq primer: M13 Reverse
Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 371)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S.,
Meller,A., Shaker,R., Furlong,J., Young,J., Zhao,S.,
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GSS.
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1 41 c
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E-Coli DH10B"
94 c 40 g 165 t
                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="Plate=3082 Col=4
/clone_lib="CIT Approved
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Pred. NO. 17;
9; Mismatches 20;
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Adams,M.D.
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Contact: Mahairas GG, Wallace JC, Hood L

Contact: Mahairas GG, Wallace JC, Hood L

High Throughput Sequencing Center

University of Washington

Iniversity of Washington and Iniversity of Washington and Iniversity of Washington.

Fax: (206) 616-3887

Fax: (206) 616-3887

Email: jwallace@t.washington.edu

Clones are derived from the human BAC library RPCI-11. For BAC

Clones are derived from the human BAC library RPCI-11. For BAC

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HS_5232_A2_H02_SP6E RPCI-11 Human Male BAC Library sapiens genomic clone Plate=808 Col=4 Row=0, genomic
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1 (bases 1 to 48")

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Mahairas,G.G., Wallace,J.C., Smith,Y., 2hao,S., Adams,M.D. and
Repler,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
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Location/Qualifiers
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Class: BAC ends
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milarity 42.5%;
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Natl. Acad. Sci. U. S. A. 96 (17), 9739-9744 (1999)
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pBACe3.6 vector at EcoRI sites

a 130 c 102 g 123 t 3 others
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/db_xref="taxon:9606"
/clone="plate=808 Col=4 Row=O"
/clone_lib="RPCI-11 Human Male BAC Library"
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Homo sapiens
                                                     AA204674.1
                                                                                                                                                                                                                                                                               Similarity 50.0
22; Conservative
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Thermostabilization and thermoactivation of thermolabile enzymes by
trehalose and its application for the synthesis of full length cDNA
(Proc. Natl. Acad. Sci. U.S.A. 95(2):520-524 (1998)
Transcriptional sequencing: A method for DNA sequencing using RNA
please (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))
Please visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RIKEN
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: 81-298-36-9145
Fax: 81-298-36-9098
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Unpublished (1999
On Jun 15, 1998 t
Contact: Chie Owa
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AV025658 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone
1200014N20, mRNA sequence.
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 378)
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Hact: Chie Owa
                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:10090"
/clone="1200014N20"
/clone_lib="Mus musculus adult C57BL/6J lung"
                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="lung"
/dev_stage="adult"
68 c 65 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Mus musculus"
/strain="C57BL/6J"
                                                   GI:1802525
                                                                                                                                                                                                                                                                                                23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                on/Qualifiers
                                                                                                                                                                                                                                                                         Score 29.6; D
Pred. No. 22;
L3; Mismatches
                                                                                                                                                                                                                                                                                                            DB 48;
                                                                                             CDNA
                                                                                                                                                                                                                                                                         9,
                                                                                           clone
                                                                                                                                                                                                                                                                                                        Length 378;
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                                                                                      13-AUG-1997
IMAGE:682670 5',
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; Murinae; Mus
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RESULT 9
AA305899/c
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AUTHORS
TITLE
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Best Local (
Eukaryota; Metazoa; Chordata; Crauter,
Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

E 1 (bases 1 to 373)

RS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Fuldner,R.A.,
Bult,C.J., Lee,N.H., Kirkness,E.F., Weinstock,K.G., Gocayne,J.D.,
White;O., Sutton,G., Blake,J.A., Brandon,R.C., Man-Wal,C.,
Claytton,R.A., Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.I,
Fitzgerald,L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S.,
Glodek,A., Gnehm,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S.,
"""" M., Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.
                                                                                                                                                                                                                                                                                                                                                                                                    200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260
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                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCCAGCTTGTTAAGAATACGGTGGAGGATCTTCAGCAGGGAGTGTCATGAGTTTCAAGT 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gcgcggcuugcgaauaauacuuuggagagucuuuugccuccagugucuuccguuuguacu 96
                                                                                                                                                                                                                                           myeloid cell different
AA305899
AA305899.1 GI:1958229
                                                                                                                                                                                                                                                                    A3305899 373 bp mRNA EST176897 Jurkat T-cells VI Homo sapiens myeloid cell differentiation protein, mRN
                                                                                                                                                                                                                   human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (1997)
Contact: Robert Stra
Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tel: (301) 490 1770
Email: Robert_Strausberg@nih.gov
This clone is available royalty-free through LLNL; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IMAGE Consortium (info@image.lin1.gov)
Seq primer: -28M13 rev2 from Amersham
High quality sequence stop: 262.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 331)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
/db_xref="GDB:5585990"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="germinal center B
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone="IMAGE:682670"
/clone_lib="NCI_CGAP_GCB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    23.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Strausberg, Ph.D
                                                                                                                                                   Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 29.4; DI
Pred. No. 25;
15; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 22;
                                                                                                                                                                                                                                                                     ens cDNA 5' end similar mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 331;
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                                                                                                      Gocayne, J.D.,
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                                                                       Fine, L.D.,
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COMMENT

JOURNAL MEDLINE

TITLE

FEATURES

source

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RESULT 10
AW219133/c
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Best Local Similarity
Matches 27; Conserv
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NE 12140200
Other_ESTs: THC171424
Contact: Kerlavage, AR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bioinformatics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850 USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index (http://www.tigr.org/tdb/hgi/hgi.html) seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 3018699423
                                                                                                                                                                  Lycopersicon esculentum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyte
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Solanales
Magnoliophyta; eudicotyledons; Asteridae; euasterids I; Solanales
Solanaceae; Solanum; Lycopersicon.

1 (bases 1 to 643)
1 (bases 1 to 643)
1 van der Hoeven,R.S., Garvin,D., Matern,A.L., Holt,I.E., Liang,F.,
Upton,J., Hansen,T., Craven,M.B., Bowman,C.L., Ahn,S.,
Upton,J., Hansen,T., Craven,M.B., Giovannoni,J.J. and
Ronning,C.M., Fraser,C.M., Martin,G.B., Giovannoni,J.J. and
                                                                                                                                                                                                                                                                                                                                                                                                              Lycopersicon esculentum AW219133 AW219133.1 GI:6530007
                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Manksley. No. 1. Transsley No. 1. (1995) Irom tomato root tissue Generation of ESTs from tomato root tissue Unpublished (1999) this sequence version replaced gi:5407336. On Jul 7, 1999 this sequence version replaced gi:5407336. Contact: David Frisch Clemson University Genomics Institute Clemson University Genomics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="ATCC (inhost):159943"
/db_xref="taxon:9606"
/clone_lib="Jurkat T-cells VI"
/cell_type="T-lymphocyte"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note "Vector: pBluescript SK-; Site_1: EcoRI; XhoI"
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Clemson,
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Cornell University
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I; Solanales;
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BASE COUNT

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269

REFERENCE AUTHORS

COMMENT

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556 GGCGGCGCCGTTCGAATTGATGGTCGAAGATGACGAAGCTGGTGAAACCGAGCCAGTCGA 497
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                                                                                                                                                                       NR. Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fuldner, R.A.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Lee, N.H., Kirkness, E.F., Weinstock, K.G., Gocayne, J.D.,
Bult, C.J., Lee, N.H., Blake, J.A., Brandon, R.C., Man-Wai, C.,
White, O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Fitzgerald, L.M., Fitzhugh, W.M., Fritchman, J.L., Geoghagen, N.S.,
Glodek, A., Gnehm, C.L., Lu, J.L., Saudek, D.M., Shirley, R.,
Woreno-Palanques, R.F., McDonald, L.A., Nguyen, D.T., Pelligrino, S.M.,
Kelley, J.M., Kelley, J.C., Utterback, T.R., Weidman, J.F., Li, Y.,
Small, K.V., Spriggs, T.A., Utterback, T.R., Weidman, J.F., Li, Y.,
Bednarik, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Dinke, D., Feng, D.-F., Ferrie, A., Fischer, C., Hastings, G.A.,
Kozak, D.L., Kunsch, C., Hungjun, J., Li, H., Meissner, P.S., Olsen, H.,
Kozak, D.L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Raymond, L., Wei, Y.F., Wing, J., Xu, C., Yu, G.L., Ruben, S.M.,
Fischer, C.M., and Venter, J.C.
Fraser, C.M. and Venter, J.C.
Fraser, C
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Fax: 864 656 4293
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EST23928 Bone marrow Homo sapi
cell differentiation protein,
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                                                                                                                   Other_ESTS: THC171424
The Institute for Genomic 9712 Medical Center Drive,
                                                              Bioinformatics
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106 c 173 g 129 t
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/clone="clex2J20"
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                                                                                                 Kerlavage,
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Homo sapiens cDNA 5' end similar to myeloid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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AW6028807

AW6028807

AW60E:2974735 3: Mar-2000

LEUKEMIA CELL DIFFERENTIATION PROTEIN MCL-1.; mRNA sequence.

AW628807

AW628807.1 GI:7375518
                                                                                                                                                                                                                                                                                                                                                                                                    On Feb 22, 1999 this sequence version replaced gi:4283533 Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1550
                                                                                                                                                                                                                                                                                                                              Possible reversed
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mammalia; Eutheria;
l (bases 1 to 256)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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27; Conservative
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For clone availability, additional sequence and expression
information related to this EST, please check the TIGR Human Gene
Index (http://www.tigr.org/tdb/hgi/hgi.html)
Seq primer: M13 Reverse.
                                                                                                                                                                                                                                                                                                       primer: -40UP from Gibco
                                                                                                                                                                                                                                                                                                           clone is available royalty-free through LLNL; contact the E Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                  quality sequence stop: 181.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5
                                                                                                                                                                                                                                                                                                                                                                         Robert_Strausberg@nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3018699423
/note="Organ: pooled; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCBI) were mixed, and secircles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made
                                                                                                                                                            /clone="IMAGE:2974735"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="bone marrow"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Bone marrow"
/sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="ATCC (inhost):122003"
/db_xref="taxon:9606"
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Pred. No. 38;
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                                                                                                                                                                                                                                                                                                                                                High quality sequence stops: 248
                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                 On Dec 20, 1995 this sequence version
                                                                                                                                                                                                                                                                                                                                                                                              Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. i
                                                                                                                                                                                                                                                                                                                                                                                                                                                             The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
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Y865ell.sl Soares retina N2b4HR Homo 
IMAGE:119692 3' similar to SP:A47476 
PRODUCT HOMOLOG - ;, mRNA sequence.
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27; Conservative
quality sequence stop: 248.
Location/Qualifiers
                                                                                                                                                                                       /db_xref="taxon:9606"
/clone="IMAGE:219692"
                                                                                                                                                                       /clone_lib="Soares retina N2b4HR"
                                                                                                                                                  /tissue_type="retina"
                                                                                                                                                                                                               /db_xref="GDB:3847685"
                                                                                                                                                                                                                          organism="Homo sapiens"
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Pred. No. 38;
9; Mismatches
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A47476 MCL1 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lennon,G., Maes,M., Tan,F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wohldmann, P. and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Watteston,R. and Wilson,R. washu-Merck EST Project 1997
Washu-Merck EST Project 1997
Unpublished (1997)
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1 (bases 1 to 285)
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Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Fal: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
Email: est@watson.wustl.edu
Email: clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
This clone is available royalty-free through LLNL; contact the
TMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -41m13 fwd. ET from Amersham
High quality sequence stop: 267.
Location/Qualifiers
1 286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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/tissue_type="ovarian tumor"
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/lab_host="DHIOB (ampicillin resistant)"
/lab_host="DHIOB (ampicillin resistant)
/note="organ: ovary; Vector: pT733 (pharmacia) with a /note="organ: ovary; Vector: poilso(ar); lsc RI; lst modified polylinker; Site_1: Not I: -0.1190(dT) primer [5/strand cDNA was primed with a Not I: -0.1190(dT) primer [5/strand cDNA was primed with a Not I: gated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI double-stranded cDNA was size selected, ligated to Eco RI adapters (pharmacia), digested with Not I and cloned into adapters (pharmacia). Library constructed by Bento Soares and (pharmacia). Library constructed by Bento Soares and M.Fatima Bonaldo. "

52 a 91 c 102 9 40 t
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85 c 98 g 42 t 1 others
                                                                                                                                                                                                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:724534"
                                                                                                                                                                                                                                                                                                                           /clone_lib="Soares ovary tumor NbHOT"
/sex="Female"
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Pred. No. 38;
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Query Match Best Local S Matches

Similarity 56... 27; Conservative

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22.7%;

Score 28.8; Pred. No. 38 Mismatches 38;

DB 23;

Length 285; Indels

12;

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Gaps

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RESULT 15
AA883427/c
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TITLE
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Search completed: August Job time: 9753 sec
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                                                                                                                   This clone is available royalty-free through LLNI; contact the IMAGE Consortium (info@image.llnl.gov) for further information. possible reversed clone: similarity on wrong strand seq primer: -40ml3 fed. ET from Amersham High quality sequence stop: 205.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    On Jan 5, 1998 this sequence version replaced gi:2581350. Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 317)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA883427.1 GI:2992957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (1997)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
                                                                                                                                                                                                                Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                      //au_invst_ probled; Vector: pT7T3D-Pac (Pharmacia) with /note*Torgan: pooled; Vector: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified polylinker; Site_1: Not I; Site_2: Eco RI; a modified plank there normalized begins reserved and B-cell libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed; and so circles were made in NCI_CGAP_GCB1) were mixed; and so circles were made in NCI_CGAP_GCB1) were mixed; and so circles were made as vitro. Following HAP purification, this DNA was used as vitro. Following HAP purification, this DNA was used as vitro. Following HAP purification, reaction. The driver tracer in a subtractive hybridization reaction. The driver tracer in a subtractive hybridization for some made was PCR amplified cDNAs from pools of 5,000 clones made was PCR amplified cDNAs from pools consisted of from the same 3 libraries. The pools consisted of IM.A.G.E. clones 297480-302087, 682632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. "
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                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9506"
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1. .317
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Pred. No. 39;
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Sequence 23, Appl Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 5, Appli Sequence 4, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 21, Appli Sequence 22, Appli Sequence 22, Appli Sequence 21, Appli

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Sequence:
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                                                score:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-28-29-270A-2
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US-08-765-662-11
US-08-765-662-11
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101.208 Million cell updates/sec
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                        Sequence 18, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 9, Appli Sequence 18, Appli Sequence 18, Appli Sequence 14, Appli Sequence 14, Appli Sequence 14, Appli Sequence 5, Appli Sequence 11, Appli Sequence 13, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli
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                                                                                                                                                                                                                                                                                                      Description
RESULT 2
US-08-077-848A-1/c
; Sequence 1, Application US/08077848A
; Patent No. 5470955
; GENERAL INFORMATION:
APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Spensley Horn Jubas & Lubitz
STREET: 1880 Century Park East, Suite 500
; CITY: Los Angeles
STATE: California
                                                                                                                                                                                                                                                                       RESULT 1

US-09-226-568-18/c

Sequence 18, Application US/09226568

Patent No. 6001992

GENERAL INFORMATION:

APPLICANT: Ackermann, Elizabeth J.

APPLICANT: Bennett, C. Frank

APPLICANT: Bennett, C. Frank

APPLICANT: Marcusson, Eric G.

TITLE OF INVENTION: Antisense Modulation of No.

FILE REFERENCE: ISPH-0337

CURRENT APPLICATION NUMBER: US/09/226,568

NUMBER OF SEQ ID NOS: 39

SOFTWARE: Patentin Ver. 2.0

LENGTH: 3934

TYPE: DNA

CORGANISM: Homo sapiens

FEATURE:

OTHER INFORMATION: Description of Artificial Secondarion of No.

US-09-226-568-18
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Best Local S
Matches 27
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US-08-910-973-1
PCT-US95-05741-1
US-08-308-881-5
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US-09-058-264-1
US-08-32-766A-11
US-08-32-766A-11
US-08-780-370A-1
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US-08-724-394A-21
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Length 3934; Indels

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COMPUTER READABLE FORM:

MEDIUM TYPE:

COUNTRY: ZIP: 900

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; OTHER INFORMATION: a
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NAME: Haile, ph.D., Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE,DOCKET NUMBER: PD-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09211640 Patent No. 6020466 GENERAL INFORMATION:
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SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,848A
FILING DATE: 16-JUN-1993
CLASSIFICATION: 424
CLASSIFICATION: 424
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LENGTH: 3946 base pairs
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MOLECULE TYPE: DI
MMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                              APPLICANT: Craig, Ruth W.
TITLE OF INVENTION: ANTIBODIES |
TITLE OF INVENTION: POLYPEPTIDE
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
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CITY: Los Angeles
STATE: California
                                                                                                                                                                                                       COUNTRY: UZIP: 90067
                                                  FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                       APPLICATION NUMBER:
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IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                       E: Spensley Horn Jubas & Lubitz
1880 Century Park East, Suite 500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                           USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note= "When nucleotide 740 = C, amino acid 227 = A; when nucleotide 740 = T, amino acid 227 = V."
                                                                                                                                                                                                                                                                                                                                                              ANTIBODIES WHICH SPECIFICALLY BIND mcl-1
                                                                                        US/09/211,640
                         08/441,375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PD-2845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 28.8;
Pred No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 3946;
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NAME/KEY: CDS
LOCATION: 61..1110
LOCATION: 61..1110
OTHER INFORMATION: //
OTHER INFORMATION: au
OTHER INFORMATION: ac
US-09-211-640-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 56.2
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
SEQUENCE 3946 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence 1, Application PC/TUS9403547 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Haile, ph.D., Lisa
REGISTRATION NUMBER: 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -US94-03547-1/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (619) 455-5100
                                                                                                                                 APPLICATION UNDER: PCT/US94/
PILING DATE: 31-MAR-1994
CLASSIFICATION: INFORMATION:
ATTORNEY_AGENT INFORMATION:
NAME: Wetherell, Jr., Ph.D.,
NAME: Wetherell, Jr., Ph.D.,
REGISTRATION NUMBER: F0-8
REFERENCE_POCKET NUMBER: F0-2
REFERENCE_TOLKET NUMBER: F0-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 455-5100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: 11
                                                                                                        TELEFAX: (619) 455-5110
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: MCL-1
                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                               STREET: 1880 Century Park East, Suite 500 CITY: Los Angeles STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
MOLECULE TYPE: DNA (genomic)
                               STRANDEDNESS: SI
                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                          90067
                                              nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The Johns Hopkins University School of Medicine VENTION: MYELOID CELL LEUKEMIA ASSOCIATED GENE
                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                               3946 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
                                                                                                                                                                                                                                                                                                                                            Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "When nucleotide 740 = C,
amino acid 227 = A; when nucleotide 740 =
acid 227 = V."
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                                                                                                                                                                                                    Ph.D., John W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PD-2845
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Pred. No. 0.4;
                                                                                                                                                                            FD-2845
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RESULT 6
US-08-484-993B-9
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; MOLECULE TYPE: DNA (genomic)
US-08-279-270A-2
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                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PCT-US94-03547-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: 512/320-7200
TELEFAX: 512/474-7577
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local :
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                                                                                                          1416 CTTCCTGTCTCTGTCTGTCCACCTCCTCCTCCTCTCCC 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA.
APPLICATION NOMER: US/08/279,270A
FILING DATE: Concurrently herewith
CLASIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mayfiala
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 33,732
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/320-7200
TELEPAX: 512/474-7577
FORMATION FOR 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                              y match 21.3%;
Local Similarity 46.5%;
hes 20; Conservative 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Mayfield, Denise L. REGISTRATION NUMBER: 33,7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  600 CTCCAGCGACTGCCGGTACAACTCGTCCTCCTCCTCCTCCTGGCGG 553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 56.2 tes 27; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 61..1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2, Application US/08279270A
o. 5691460
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 single
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amino acid 227 = A; when nucleotide 740 = T, amino
acid 227 = V."
                                                                                                                                                                                                                                              13;
                                                                                                                                                                                                                                 Score 27; DB 2; Length 2488;
Pred. No. 1.5;
3; Mismatches 10; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 28.8;
Pred. No. 0.
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; LOCATION:
US-08-484-993B-9
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HYPOTHETICAL: NV
ANTI-SENSE: NO
ORIGINAL SOURCE: OTHER SOURCE:
ORGANISM: Canis familiaris
DEVELOPMENTAL STAGE: Juvenil
HAPLOTYPE: Diploidy
"TSSUE TYPE: Ovary
Occyte
                                                                                                                                      Query Match
Best Local Similarity
Matches 31; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424

PRIOR APPLICATION DATA:
APPLICATION UNMER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION UNMER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, DAVId W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 9, Application US/08484993B Patent No. 5837497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
1670 CCACTTGCCTTAATCCTGC 1688
                                                            1610 CTGCTGATAAATACCAATGTCCAAAGTCTTCCTCCTCCCTGGCCTCAGTGAGGCCTGGT 1669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Harris Ph.I
APPLICANT: Hsu, Kuang
APPLICANT: Podolski,
                               100 ccuccucucccucuccggc 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,993B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                               40 cggcuugcgaauaauacuuuggagagucuuuugccuccagugucuuccguuuguacucgu 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: doub
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 6300 Sea:
CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RY: United States of America
60606-6402
                                                                                                                                        Conservative
                                                                                                                                                                                                                                        CDS
206..2353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         E: Marshall, O'Toole, Gerstein, Murray & 6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Podolski, Joseph S.
VENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harris Ph.D., Jeffrey D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09-NOV-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      double
                                                                                                                                                     20.6%;
                                                                                                                                                                                                                                                                                                                                                 Juvenile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US/08/484,993B
                                                                                                                                      15;
                                                                                                                                                   Score 26.2; DB Pred. No. 2.8;
                                                                                                                                      Mismatches
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••
                                                                                                                                                                  Length 2381;
                                                                                                                                  Indels
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                                                                                                                             Gaps
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RESULT

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US-08-484-158B-9
                                                                                                                        ; NAME/KEY:
; LOCATION:
US-08-484-158B-9
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                                                       Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                  NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/973,341 FILING DATE: 09-NOV-92 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Pharmaceutical Comporting OF INVENTION: Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08
FILING DATE: 29-JAN-93
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: 312/474-6653
TELEPHONE: 312/474-0448
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                               TOPOLOGY: lines
MOLECULE TYPE: CI
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                       ORIGINAL SOURCE:
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                                                                                                                                                                                                                                                                     NTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/
FILING DATE: 07-JUNE-95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
              40 cggcuugcgaauaauacuuuggagagucuuugccuccagugucuuccguuuguacucgu 99
                                                                                                                                                                                   CELL TYPE:
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                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clough, David W.
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                                                                      Similarity
                                                                                                                                                                                                                                                                                                                         nucleic acid
EDNESS: double
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Podolski,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harris Ph.D., Jeffrey
                                                                                                                                                                                                                                                                                                                                                       2381 base pairs
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206..2353
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E: Ovary
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                                                                                                                                                                                    Oocyte
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                                                          Score 26.2; D. Pred. No. 2.8; 15; Mismatches
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                                                                                      DB 4;
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Patent No. 5981228
Query Match
Best Local Similarity
Matches 31; Conserv
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INFORMATION FOR SEQ ID NO:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PROCOMPOSITION
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
COFFWARE: Patentin Release #1.0, Version #1.25
SOFFWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/484,596A
APPLICATION NUMBER: US/08/484,596A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 59
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 07/9;
FILING DATE: 09-NOV-1992
ATTORNEY_AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/1.
FILING DATE: 11-NOV-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pair
                                                                                                                                                                                                                                   ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States ZIP: 60606-6402
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31:
                                                                                                    NAME/KEY:
                                                                                                                                                                 DEVELOPMENTAL STAGE:
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
                                                                                                                                                                                                                                                                                                                  STRANDEDNESS:
                                                                                                                                                     CELL TYPE:
                                                                                                                                                                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                                                                       ORGANISM:
                                                                                                                                                                                                                                                                                                                                   nucleic acid
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6300 Sears Tower, 233 South Wacker Drive
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Podolski, Joseph S.
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        Score 26.2; D. Pred. No. 2.8; 15; Mismatches
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                                           Length 2381;
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US-08-480-150A-9
   Ouery Match 20.6%;
Best Local Similarity 39.2%;
Matches 31; Conservative 1
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CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/149,223
APPLICATION NUMBER: US 08/149,223
APPLICATION NUMBER: 08/012,990
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
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                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 25-3856
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                            DEVELOPMENTAL STAGE:
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
CELL TYPE: Occyte
                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6653
TELEFAX: 312/474-0448
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAtentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APDT TOATTON MINISTED: HC //8 //80 1501
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HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: 07/97 FILING DATE: 09-NOV-1992 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: doub
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/480,150A
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE
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5. 5989550
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                                                                                                                                                                                                                                                                                                                                                                                2381 base pairs
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6300 Sears Tower, 233 South Wacker Drive
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Podolski, Joseph S.
VENTION: Materials and Methods for Immunocontraception
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                                                                                                                 CDS
206..2353
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                    Score 26.2;
Pred. No. 2
     Mismatches
                                       DB
   33;
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                                   Length 2381;
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; NAME/KEY:
; LOCATION:
US-08-458-731-9
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                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/012
FILING DATE: 29-TAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
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                                                   FEATURE:
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                                                                                                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,731
                                                                                                                                                            HYPOTHETICAL:
                                                                                                                                                                                         MOLECULE TYPE:
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
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                                                                           ORGANISM: Canis familiaris
DEVELOPMENTAL STAGE: Juvend
HAPLOTYPE: Diploidy
TISSUE TYPE: Ovary
                                                                                                                                                                                                                                                                                                     12/474-6653
TELEFAX: 312/474-0448
TELEX: 25-3856
                                                                                                                                                                                                              TOPOLOGY: 11
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CITY: Chicago
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: United States of America ZIP: 60606-6402
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                                                                TYPE:
                                                                                                                                                                                                                                         nucleic acid
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               CDS
206..2353
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Podolski, Joseph S.
VENTION: Materials and Methods for Immunocontraception
                                                                                                                                                                                                            linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Harris Ph.D., Jeffrey
                                                             Oocyte
                                                                                                                                                                                             CDNA
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                                                                                                                                                                                                                            double
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                                                                                                           Juvenile
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Query Match 20.6
Best Local Similarity 39.2
Matches 31; Conservative

20.6%;

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Score 26.2; DE Pred. No. 2.8; 15; Mismatches

DB 5; 33;

Length 2381; Indels

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1610 CTGCTGATAAATACCAATGTCCAAAGTCTTCCTCCTCCCTGGCCTCAGTGAGGCCTGGT 1669

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Query Match
Best_Local Similarity
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/012,990
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/973,341
FILING DATE: 09-NOV-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                     TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 9
SEQUENCE CHARACTERISTICS:
LENGTH: 2381 base pairs
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/149,223A
FILING DATE: 09-NOV-1993
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE, DOCKET NUMBER: 31
TELECOMMUNICATION INFORMATION:
                                                                                                               FEATURE:
                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                        MOLECULE TYPE: CI
                                                                                                                                                                                                                        ANTI-SENSE:
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CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                       TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX:
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                                                                                                                               CELL TYPE:
                                                                                                                                            HAPLOTYPE: 1
TISSUE TYPE:
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                                                                                                NAME/KEY:
                                                                                  LOCATION:
                                                                                                                                                                              DEVELOPMENTAL STAGE:
                                                                                                                                                                                             ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        60606-6402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Application US/08149223A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E: Marshall, O'Toole, 6300 Sears Tower, 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hsu, Kuang
Podolski, J
                                                                                                                                                                                                                                                                                                                                                                                    312/474-6653
312/474-0448
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                                                                                                                                              Diploidy
E: Ovary
                                                                                                                                                                                                                                                                         linear
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                                                                                                CDS
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                                                                                                                               Oocyte
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   20.6%;
                                                                                                                                                                                Juvenile
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      Score
Pred.
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     26.2; DB
No. 2.8;
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                       Length 2381;
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RESULT

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US-08-480-552-18/c
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Patent No. 5665550
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PRIOR APPLICATION LATA: 435
PRIOR APPLICATION NUMBER: US 08/033,086
APPLICATION NUMBER: US 08/033,086
APPLICATION NUMBER: US 08/033,086
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                                                                                                                                                Query Match
Best Local Similarity
Matches 27; Conserv
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pair:
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TITLE OF INVENTION: Genes And Genetic Elements Associated
TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Allegretti & Witcoff, Ltd
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Keown, Wayne A.
REGISTRATION NUMBER: 33,923
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/345-9100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                                                          1296 ATATTCCTTTGTTTTTGTCTTCAACTTCCTGAGACTTCTGATCATAATTAACAGCCAGTTC 1237
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1236 CTCTAAGGCCTGTA 1223
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                                110 cucuccggccggga 123
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STATE: Massa
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TELEPHONE: or//
617/345-9111
TO ID NO:
                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
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36.5%;
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                                                                                                                                                            Score 26; DB Pred. No. 3.3; Nismatches
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US-08-486-382-4/c

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                                                                                                                                                      Sequence 4, Application US/09235546 Patent No. 6043340
                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches 27; Conserv
                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 2389 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 4, Application US/08486382 Patent No. 5866327
                                 APPLICANT: Gudkov, Anarei
APPLICANT: Gudkov, Anarei
APPLICANT: Roninson, Igor B.
TITLE OF INVENTION: Association of Kinesin with Sensitivity
TITLE OF INVENTION: To Chemotherapeutic Drugs
                                                                                                                                                                                                                                                    1236 CTCTAAGGCCTGTA 1223
                                                                                                                                                                                                                                                                                                            1296 ATATTCCTTTGTTTTTGTCTTCAACTTCCTGAGACTTCTGATCATAATTAACAGCCAGTTC 1237
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 312/715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US 08/177,571
FILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: No. 5866327nan, Kevin E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Association of Kinesin with Sensitivity
TITLE OF INVENTION: To Chemotherapeutic Drugs
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gudkov, Ar
ADDRESSEE: Allegretti & Witcoff, Ltd
STREET: 75 State Street
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STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: NO. 5866327nan, Kevin
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/486,382
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36.5%; Pred. No. 3
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RESULT 15
US-08-29-208-18/c
; Sequence 18, Application US/08929208
; Patent No. 6060244
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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Best Local :
         COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/177,57
ETILING DATE: 05 JAN 1994
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6043340nan, Kevin E.
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 93,354-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          TITLE OF INVENTION: Genes And Genetic Elements Associated TITLE OF INVENTION: With Sensitivity To Chemotherapeutic Drugs NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1296 ATATTCCTTTGTTTTGTCTTCAACTTCCTGAGACTTCTGATCATAATTAACAGCCAGTTC 1237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1236 CTCTAAGGCCTGTA 1223
                                                                                                                                                                                                                                                                                                  APPLICANT: Gudkov, Andrei
APPLICANT: Roninson, Igor
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/235,546
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TELEPHONE: 312/715-1000
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 APPLICATION NUMBER:
                                                                                                                                                                  CITY: Boston
STATE: Massa
                                                                                                                                                                                        ADDRESSEE: Allegretti & Witcoff, Ltd STREET: 75 State Street
                                                                                                                                             COUNTRY:
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TOPOLOGY: 11r
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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05 JAN 1994
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US/08/929,208
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Page 8
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CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/480,552
FILING DATE:
FILING DATE:
ATTORNEY/ACENT IMPORMATION:
AME: RESERVED/DOCKET NUMBER: 33,923
RESISTRATION NUMBER: 33,923
RESISTRATION NUMBER: 93,334
TELECOMMUNICATION INFORMATION:
ATTELEPHONE: 617/345-9110
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 Dase pairs
TYPE: CONA
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 238 Dase pairs
TYPE: CONA
STRANDEDNESS: Single
TYPE: CONA
HIPOTHETICAL: NO
ANTI-SENSE: YES
US-08-929-208-18

Ouery Match
HIPOTHETICAL: NO
ANTI-SENSE: YES
US-08-929-208-18

Ouery Match
Sept Local Similarity 36.5%; Pred. No. 3.3;
Matches 27; Conservative 1::: | I | I | I |
DATE ANATYCCTTTGTTTTGTCTTCAACTTCCTGAGCTAATTAACAGCCAGTTC 1237

Oy 110 cucucc99c9gga 123
Db 1126 ATATYCCTTAAGCCTGTA 1223

Search completed: August 7, 2000, 09:28:57
Job time: 911 sec
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	Database :	Post-processing:	Minimum DB seq 1 Maximum DB seq 1	Total number of	Searched:	Scoring table:	Title: Perfect score: Sequence:	Run on:	eic -	
1: em_estl:* 2: em_est2:* 4: em_est4:* 4: em_est6:* 5: em_est6:* 7: em_est10:* 11: em_est10:* 11: em_est11:* 11: em_est11:* 11: em_est11:* 11: em_est15:* 15: em_est15:* 16: em_est15:* 17: em_est15:* 18: em_est16:* 19: em_est11:* 11: em_est11:* 11: em_est11:* 12: gb_est1:* 13: gb_est1:* 14: gb_est1:* 15: gb_est1:* 16: gb_est1:* 17: gb_est1:* 18: gb_est1:* 19: gb_est1:* 19: gb_est1:* 19: gb_est1:* 19: gb_est1:* 10: gb_est1:* 11: gb_est1:* 11: gb_est1:* 12: gb_est1:* 13: gb_est1:* 13: gb_est1:* 14: gb_est1:* 15: gb_est1:* 16: gb_est1:* 17: gb_est1:* 18: gb_est1:* 19: gb_est1:* 19: gb_est1:* 19: gb_est1:* 10: gb_est1:* 11: gb_es	,	: Minimum Match 08 Maximum Match 1008 Listing first 45 summarles	seq length: 0 seq length: 1000000	of hits satisfying chosen parameters: 10495684	5247842 segs, 2204914090 residues	IDENTITY_NUC Gapop 10.0 , Gapext 1.0	US-09-214-124-2_COPY_265_578 314 1 gguaccucgcgaggguuuggcccucuccggccgggauggg 314	August 7, 2000, 11:56:08; Search time 3871.63 Seconds (without alignments) 357.649 Million cell updates/sec	nucleic search, using sw model	GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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Result No. a

Score

% Query Match

Length

DB

39.4 37.6 36.8 35.4 35.2

34.8

Pred. No. 15 c score greater

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Insecta;

sequencage : scope.cns.fr

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CNS0119V 807 bp DNA GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence T7 end of BAC BACNO5C05 of DrosBAC library from Drosophila melanogaster (fruit
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ALIOS077 Drosophil
ALIOS085 Drosophil
ALIOS38 Drosophil
AA767466 ob46f03.s
AA440840 LDI5761.5
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ALIOS040 Drosophil
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ALIOS090 Drosophil
ALIOS0912 Drosophil
ALIOS0912 Drosophil
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AI322633 mj07b01.y
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AL050564 Drosophil
AL057398 Drosophil
AL106438 Drosophil
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre
BP 191 91006 EVRY cedex - FRANCE (E-mail:
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                          fruit fly.

Drosophila melanogaster

Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins

Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;

Pterygota; Neoptera; Endopterygota; Diptera; Drosophila.

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 1101)
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/db_xref="taxon:722"
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Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr | Web : www.genoscope.cns.fr | Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osocgawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BACR14J09 of RPCI-98 library from Drosophila melanogaster (fruit
fly), genomic survey sequence
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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/clone="BACN17J04"
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Web: www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Aaron Mammoser in Pleter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

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/db_xref="taxon:7227"
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Osoegawa and Maron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCI-98 and was constructed by partial EcoRI digestion of Drosophila DNA provided by the BDGP from the isogenic strain y2; on bw sp. the same strain used for the BDGP's pl and EST libraries. A more detailed description of the library and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Ins
Eukaryota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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BP 191 91006 EVRY cedex - FRANCE (E-mail : seqrefégenoscope.cns.fr
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/db_xref="taxon:7227"
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/clone="BACR14J21"
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63 c 112 g 198 t 335
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). This://www.edgp.ebi.ac.uk. This Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk. Billaud at CEPH (Centre Ilbrary (Dros BAC) was made by Alain Billaud at CEPH (Centre G'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage :
BP 191 91006 BVRY cedex - FRANCE (B-mail : segref@genoscope.cns.fr
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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Score 35.2; DE Pred. No. 4.2; 69; Mismatches
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                                                                                              GGSSSCGCGGGGRGSGTKAAAAARRRRGARGARAGRWGTGAGARRRTGAKTTTTTTTTTTT
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Pterygota; Meoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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91 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
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/clone="BACNO3M23"
/note="end: T7"
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19.8%; Pred. No. 4.2;
ative 62; Mismatches
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:| ::
988 NTCTTT
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Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP).

The BDGP is constructing a physical map of the Drosophila please see http://www.fruitfly.org The BDGP Drosophila please see http://www.fruitfly.org The BDGP Drosophila naron Mammoser in Pieter de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, Ecori digestion of Drosophila DNA provided by partial isogenic strain y2; cn bw sp, the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be Location/Qualifiers

Location/Qualifiers
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                                                                                                                                  Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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fly), genomic survey sequence.
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AL107151.1 GI:5625839
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Genoscope.

Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage : Submitted (23-JUL-1999) Genoscope - Centre National : seqref@genoscope.cns.fr Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Bp 191 91006 EVRY cedex - Chis BaC-end sequence was carried out as part of a Determination of this BAC-end sequence was carried out as part of a Determination with the European Drosophila Genome Project EDGP) - Collaboration with the European Drosophila melanogaster BAC http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC http:/
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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Muscomorpha; Ephydroidea; Drosophilidae; Drosophila
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                                                                 Drosophila melanogaster
Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101)
                                                                                                                                                                                                                                                AL098851.1
                                                                                                                                                                                                   fruit fly.
  Submitted
                          Direct
                                                  Genoscope.
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nilarity 13.6%;
Conservative 11
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/db_xref="taxon:7227"
/clone_lib="RPCI-98"
/clone="BACR14B21"
                               Submission
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115 c 87 g
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5%; Pred. No. 6.2;
119; Mismatches
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             Centre National de Sequencage
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melanogaster (fruit
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                                                     AL Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the Drosophila melanogaster genome using these BACs. For further information please see http://www.fruitfly.org The BDGP Drosophila aron melanogaster BAC library was prepared by Kazutoyo Osoegawa and Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, EcoRI digestion of Drosophila DNY. The library is named RPCI-98 and was constructed by partial isogenic strain y2; cn bw sp. the same strain used for the BDGP's and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be constructed by partial places. The providual back of the BDGP from the pland EST libraries. A more detailed description of the library filters for hybridization from the BACPAC Resource Center can be constructed by partial and how to order individual BAC clones, the entire library or filters for hybridization from the BACPAC Resource Center can be constructed by the BDGP.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Inse
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 844)
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AL056652.1 GI:4932342
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Drosophila melanogaster genome survey sequence TET3 end of BAC #
BACRILP16 of RPCI-98 library from Drosophila melanogaster (fruit
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Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP) - http://www.edgp.ebi.ac.uk - This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEBH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector
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/plasmid-"pBeloBAC11"
/db_xref-"taxon:7227"
/clone_lib-"DrosBAC"
/clone-"BACNO3K12"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Ptarygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage
BP 191 9106 EVRY cedex - FRANCE (E-mail : segref@genoscope.cns.fr
Web : www.genoscope.cns.fr)
                              Similarity
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24; Conservative
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/plasmid="pBeloBaC11"
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/clone="BACN15A09"
/note="end: T7"
239 c 292 g
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/clone="BACR11P16"
/note="end : TET3"
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                       10.8%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       www-bio.llnl.gov/bbrp/image/image.html
Seg primer: -40UP from Gibco
High quality sequence stop: 283.
Location/Qualifiers
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Emmert-Buck, M.D., Ph.D.
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Tissue Procurement: Christopher Moskaluk, M.D., Ph.D.,
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CDNA Library Arrayed by: Greg Lennon, Ph.D.
CDNA Sequencing by: Washington University Genome Sequencing
DNA Sequencing by: Washington University Genome Sequencing
Clone distribution: NCI-CGAP clone distribution information
Clone distribution: NCI-CGAP clone distribution information
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                                                                                                                  Similarity 31.55; Conservative
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/tissue_type="renal cell tumor"
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ob_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville,
Tel: 301 838 0200
Fax: 301 838 0208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Other_GSSs: CIT-HSP-2345012.TF
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Class: BAC ends.
                                                                                                                                                                                                                                                                                                                                                          http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.
                                                                                                                                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
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                                                                                                         Conservative
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                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="2345012"
/clone_lib="CIT-HSP"
/sex="Male"
                                                                                                                                                                                    /cell_type="Sperm"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Gabus-Darlix,C. and Darlix,J.
GABUS-DARLIX,C. and DARLIX,J.
INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING
PATENT: WO 9849334-A 05-NOV-1998;
PATENT: WO 9849334-A 05-NOV-1998;
GABUS DARLIX CAROLINE (FR); INST NAT SANTE RECH MED (FR)
LOCATION/QUALIFIERS
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Viruses; Retroid viruses; Retroviridae; Mammalian type
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Gabus-Darlix,C. and Darlix,J.
Gabus-Darlix,C. and Dorlix SITE AND VECTOR CONTAINING NOVEL INTERNAL RIBOSOME ENTRY SITE AND VECTOR CONTAINING PATENT: WO 9849334-A 05-NOV-1998;
PATENT CARCLINE (FR; INST NAT SANTE RECH MED (FR)
GABUS DARLIX CARCLINE (FR; INST NAT SANTE RECH MED (FR)
LOCATION/Qualifiers
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Hertig.C. Coupar.B.E., Gould,A.R. and Boyle,D.B.
Field and vaccine strains of fowlpox virus carry integrated sequences from the avian retrovirus, reticuloendotheliosis virus virology 235 (2), 367-376 (1997)
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/strain="TYPE A (REV-A)"
/isolate="LEADER 5' DE L'ARN GENOMIQUE REV-A"
/db_xref="taxon:11636" 265 t
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/db_xref="taxon:10261"
/note="standard vaccine strain from Cyanamid-Webster
Ltd, Castle Hill, New South Wales, Australia.
ECORILPStI 4.3kb fragment from the 9.8kb PstI genome
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                                                                                                                                                                                 GGATGGG 1816
integration site; provirus; terminal repeat.
Spleen necrosis virus
Spleen necrosis virus
Viruses; Retroviridae; Mammalian type C
                                                       RESNVX 1530 bp DNA Spleen necrosis virus sequence 1.92Kbp from the 5' end. v01200 J02387 v01200 J G1:61757
                                                                                                                                                                                                                                                                                                                                         90;
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LEMPTFGYGMPKEGTLDFRVYDAAVRNIYGGNFGHDOVIYITWHDITIERPKYLKDC
GCKPTGPSKYLLASGKUNDRRRVLJPSAAPESPFRRMRRAGFLDERPLSPAAPEPPPPPPPPPPPPPPPPPPAIAEGEEGEGOOPDSTVMASPPHTRSGLEFGAGGPSGMYPLRETGERBUNGGRBWATYV
PTTSDLYNMEMONPSFSQAPDEVISLLESUTYTHOPTWDDCOGLARTLFTTEERERV
RTESRREVRUNDGGVQVTDERREIEAGFPATRFDWDPNTGRUDNLERYRGILLRGLRAA
RAKPTNLSKITEVROGADESPTAYLERLYQAYTWSPIDFRAPENQAAIVJDFVGGSA
PDIRKKIGKIGFGGKSLSELVAIAGKVFDQREDPAKATHELTGKMAKVLLAGESRAE

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/gene="gag"
1812. .3311
/gene="gag"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGSKKTPPGKGRPPLGKNQCAYCKEEGHWKKNCPKLVSGATPVLVEELQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="protease/polymerase"
/protein_id="AAC58240.1"
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FIEISMORCFSIKSVTDSTVLYIENRTNRYSISTSHDKNEPYEENGIIMNNIECYFVA
CLEGSCTVNVALGDRO, SDNISESSCFLMDVNTDHVIDTKYVGLFITKIKVDAHVFYG
ONVIMFPEKNLFSQTN. PNFILYDITVQDRNVLLLITSKYIYNLCDDKYYDIFELKYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VDNCKLPMPLIPLSKYDFTFTDLSVIKSENVKTVLSKVHTSMKSYYNNDTSLPVAVKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="hypothetical protein"
/protein_id="AAC58238.1"
/db_xref="GI:2393893"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'protein_id="AAC58239.1"
'db_xref="GI:2393894"
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Pred. No. 7.5e-29;
6; Mismatches 1
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Q'Rear,J.J. and Temin,H.M.

Spontaneous changes in nucleotide sequence in provirum necrosis virus, an avian retrovirus

Proc. Nati. Acad. Sci. U.S.A. 79 (4), 1230-1234 (1988, 82174569)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   retroviruses; 1-Mammalian type C virus group.
1 (bases 2 to 470)
Shimotohno,K., Mizutani,S. and Temin,H.M.
sequence of retrovirus provirus resembles tha
transposable elements
Mature + 285 (5766), 550-554 (1980)
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                                                                                                                                                                                                                                                                                         /GL_xref-"SWISS-PROT: PO3342"

/GL_xref-"SWISS-PROT: PO3342"

/translation="MGQAGSKGLLTPLECILKNFSDFKKRAGDYGEDVDSFALRKLCE
LEWPTFCYGWPKEGTLDFKYVAAVRNIYFGNPOHPDOVIYITWTDITIERFKYLKSC
GCKPHRTSKVLLASQKYMDRREVLPSAPESPBTAIRRAGFLDERPLSPAPAPPPPPEV
SAIVEDTREGQOPDSTVMTSPPHTRSGLEFGAGGPSGMYPLRETGERDMTYC
PFTTSDLYNWKKONPSSFSQAPDQVISLLESVEYTHQPTWDDCQQLLRTLFTTEERER
VRTESRREVRNDQGVQVTDEREIEAQFPATRPDWVGS"
/note="additional C in clone 3-73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="G
592. .>15
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                                       /note="A is G
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                                                                                                                                                                                           note="substitute with 135-188"
                                                                                                                                                                                                                                                                   /note="G is A in clone 63"
                                                                                                                                                                                                                                                                                                                                                                                                                                         /protein_id="CAA24513.1"
/db_xref="GI:61758"
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/db_xref="taxon:11836"
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* NOTE: This is a 'unfinished' sequence. It currently * consists of 25 conflys. The true order of the pieces is * not known and their order in this sequence record is * arbitrary. Where the conflys adjacent to the vector can * be identified, they are labelled with 'clone_end' in the * feature table. Some order and orientation information * can tentatively be deduced from paired sequencing reads * which have been identified to span the gap between two * conflys. These are labelled as part of the same * 'fragment_chain', and the order and relative orientation * of the pieces within a fragment_chain is reflected in * this file. Gaps between the conflys are represented as * runs of N, but the exact sizes of the gaps are unknown. * This record will be updated with the finished sequence as * soon as it is available and the accession number will be * preserved.
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Homo sapiens chromosome 9 clone RP11-40A7, '
PROGRESS ***, in unordered pieces.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Assembly program: XGAP4; version 4.5
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; L08752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 147679 bases at least Q40
Consensus quality: 158044 bases at least Q30
Consensus quality: 164046 bases at least Q20
Consensus quality: 164046 bases at least Q20
Insert size: 169678; sum-of-contigs
Insert size: 185740; 5.2% error; agarose-fp
Quality coverage: 2.78x in Q20 bases; sum-of-contigs Quality
Coverage: 2.54x in Q20 bases; agarose-fp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (19-APR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk on Apr 22, 2000 this sequence version replaced gi:7242470.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
1 (bases 1 to 172078)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: humquery@sanger.ac.uk
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pred. No. 2.5e-27;
4; Mismatches 4;
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166060
168182
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26595 conting of 53798 bp in length; fragment_chain 1 *
32004 conting of 5309 bp in length; fragment_chain 2 *
33672 conting of 1568 bp in length; fragment_chain 2 *
55315 conting of 21543 bp in length; fragment_chain 2 *
64000 conting of 20187 bp in length; fragment_chain 3 *
84287 conting of 20187 bp in length; fragment_chain 4 *
9429 conting of 10042 bp in length; fragment_chain 4 *
101800 conting of 10157 bp in length; fragment_chain 5 *
1015700 conting of 13800 bp in length; fragment_chain 5 *
115700 conting of 13800 bp in length; fragment_chain 6 *
115700 conting of 13800 bp in length; fragment_chain 6 *
115701 conting of 13800 bp in length; fragment_chain 6 *
115701 conting of 13800 bp in length; fragment_chain 6 *
115702 conting of 1397 bp in length
13011 134530 conting of 1397 bp in length
131911 134530 conting of 1397 bp in length
131911 134530 conting of 2015 bp in length
136131 136715 conting of 2015 bp in length
136131 136915 conting of 2015 bp in length
136141 136240 conting of 14174 bp in length
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fragment_chain:2"
33773. .55315
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/db_xref="taxon:9606"
/chromosome="9"
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94530. .100643
/note="assembly_fragment:00646
fragment_chain:5"
                                                                                                         84388. .94429
/note="assembly_fragment:00936
fragment_chain:4"
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/note="assembly_fragment:00472
fragment_chain:4"
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fragment_chain:1"
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fragment_chain:1"
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/clone_lib="RPCI-11.1"
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fragment_chain:1"
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fragment_chain:1"
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fragment_chain:3"
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fragment_chain:3"
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fragment_chain:2"
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misc_feature

/notes "assembly_fragment:00838 fragment_chain:6" 115801. .128423 /note="assembly_fragment:00555
fragment_chain:5"
101901..115700

.101800

131914. .134530 /note-"assembly_fragment:00724" 134631. .136715 /note-"assembly_fragment:00779" 136816. .160989

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note-"assembl

Y_fragment:00430'

misc_feature misc_feature

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contig_ID: 00104 Length: 2013bp
contig_ID: 00117 Length: 2013bp
contig_ID: 00129 Length: 3817bp
contig_ID: 00129 Length: 3817bp
contig_ID: 00139 Length: 3817bp
contig_ID: 00139 Length: 375lbp
contig_ID: 00139 Length: 1328bp
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contig_ID: 00297 Length: 1528bp
contig_ID: 00297 Length: 1528bp
contig_ID: 00267 Length: 1528bp
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contig_ID: 00270 Length: 1528bp
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contig_ID: 00346 Length: 1528bp
contig_ID: 00346 Length: 1528bp
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contig_ID: 00480 Length: 1528bp
contig_ID: 00554 Length: 1528bp
contig_ID: 00554 Length: 1528bp
contig_ID: 00554 Length: 1135bp
contig_ID: 00676 Length: 1501bp
contig_ID: 00676 Length: 1501bp
contig_ID: 00677 Length: 1501bp
contig_ID: 00676 Length: 1501bp
contig_ID: 00676 Length: 1501bp
contig_ID: 00766 Length: 1501b
5345: contig of 5345 bp in length
6146 7474: contig of 1329 bp in length
6146 7474: contig of 1329 bp in length
7475 8274: gap of 800 bp
9447 10246: gap of 800 bp
10247 1283: contig of 2037 bp in length
1284 13083: gap of 800 bp
13084 13083: gap of 159.6 bp in length
13084 13999: contig of 591.6 bp in length
19000 19799: gap of 800 bp
21848 22647: contig of 2048 bp in length
22648 22647: gap of 800 bp
23648 27264: gap of 800 bp
31025 31025: contig of 3761 bp in length
33351: contig of 3761 bp in length
33352 34151: gap of 800 bp
34152 36274: contig of 1236 bp in length
334152 36274: contig of 3733 bp in length
336275: 37074: gap of 800 bp
36275: 37074: gap of 800 bp
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REFERENCE AUTHORS TITLE JOURNAL

Direct Submission

Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates; 1 (bases 1 to 187155) Plumb,B.

Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.

ACCESSION VERSION KEYWORDS

SOURCE

ORGANISM

Homo sapiens

HTG; HTGS_PHASE1.

RESULT 6 AL160271/c

DEFINITION

AL160271 187155 bp D Homo sapiens chromosome 9 SEQUENCING IN PROGRESS ** AL160271 GI:7242465

DNA HTG 13-MAR-2000 9 clone RP11-323H21 map q34.1-34.3, ***
***, 46 unordered pieces.

BASE COUNT ORIGIN

43397

ß

vector_side:right" 42308 c 42354 g clone_end:T7

g

41607 t 2412 others

/note="assembly_fragment:00506 /note="assembly_fragment:01051 168182. .172078

misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature misc_feature

166060. .16808ī

'note-"assembl note-"assemb]

ty_fragment:00897" Ly_fragment:00827

164523.

/note="assembly_fragment:00825" 162441. .164422

162340

Query Match Best Local S Matches 33

Similarity 37.5 33; Conservative

25.2%; Score 32; DB 40; Length 172078; 37.5%; Pred. No. 5.4; tive 20; Mismatches 35; Indels 0;

0,

Gaps

0

COMMENT

Submitted (11-MAR-2000) Sanger Centre, Hinxton, Cambridgeshire, CB10 ISA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
IMPORTANT: This sequence is unfinished and does not necessarily progress and the release of this data is based on the understanding that the sequence may change as work continues. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector, phage etc. Order of segments is not known; 800 n's separate segments. Contig_ID: 00010 Length: 5345bp

Gaps

0;

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74471
80549 81348: gap
95658:
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184382 185181:
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41438: gap of 800 bp
43421: contig of 1983 bp in
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55542: contig of 1
76342: gap of 60520: 7
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12532: contig of 1903 bp in 1
12333: gap of 800 bp
123332: gap of 800 bp in 1
125601: contig of 2269 bp in 1c
126401: gap of 800 bp
131313: contig of 2369 bp in 1c
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: gap of
51269:
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126401: gap of 800 bp
131313: contry of 4912 bp in length
131313: gap of 800 bp
133584: contry of 1471 bp in length
134384: gap of 800 bp
137197: contry of 2813 bp in length
137197: gap of 2813 bp in length
139197: gap of 1135 bp in length
139197: gap of 6713 bp in length
139197: gap of 6713 bp in length
139197: gap of 6713 bp in length
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109306: contig of 1163 bp in length
10106: gap of 800 bp
119829: contig of 9723 bp in length
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                              187155: conti
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4: contig of 2610 bp in length
gap of 800 bp
4: contig of 2010 bp in length
gap of 800 bp
5: contig of 4541 bp in length
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contig of 1016 bp
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AUTHORS
TITLE
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                            gene
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                                                                                                                                                                                                                                                                                                                                                                            CDS
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Sorrentino, V.
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Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 1508)
1 (ba
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G.gallus mRNA for x95267
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Submitted (18-JAN-1996) V. Sorrentino, DIBIT, San Raffaele Submitted (18-type Via Olgettina 58, I-20132, Milano, ITALY Scientific Inst., via Olgettina 58, I-20132, Milano, ITALY Location/Qualifiers
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                        .1 GI:1212911
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/clone="RP11-323H21"
/clone_lib="RPCI-11.2"
/s8143 c 37226 g 38069 t
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                                                              /gene="RyR3"
78. 14687
                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="brain"
78. .14687
                                                                                                                                                                                                                                                                                                                                                                                                                                                  organism="Gallus gallus"/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                           /gene="RyR3"
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Pred. No.
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FEATURES

source

4713 a 2814 c 3374 g 4186 t 2 others

Query Match Best Local Similarity

23.8%; 47.1%;

Score 30.2; Pred. No. 27;

DB 34;

Length 3176

BASE COUNT ORIGIN

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BASE COUNT
ORIGIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 (bases 1 to 3176)
MCColl.G. and McKechnie, S.W.
Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AF096275
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                                                                                 /Product-"heat shock protein 68"
/protein_id-"AAD16140.1"
/protein_id-"AAD16140.1"
/db_xref-"G1:432942"
/translation-"mpaigidlgttySCVGVFQYGKVEIIANDQGNRTTPSYVAFTDS
ERLIGDAAKNQVAMNPKNSVFDAKRLIGARFDDSKLOEDIKHWPFKVINDNGKPKISV
FRGANKCFSPEEISSWYLTKHKETAEAYLGTTVKDAVITVPAYFNDSQRQATKDAGA
IAGINVLRIINEPTAAALAYGLDKNLKGETREAYLFDLGGGTFDVSILTIDEGGSLFEVR
IAGINVLRIINEPTAAALAYGLDKNLKGERNVLFDLGGGTFDVSILTIDEGGSLFEVR
STAGDTHLGGEDFDNRLVNHFAEEFKRXYKKDLTSRNERALRILATAAERAKRISSST
FRASLEIDALYEGHDFYSKVSRAFFEELCGDLFRNTLEPVEKALKDAKMDKSQIHDIVL
VGGSTRLFKVQNLLQNFFGGKFTLNLSINPDEAVAYGAAIDAAILSGDKSSEIKDVLLV
DVAPLSLGIETAGGVMTKLIERNSRIPCKOSKTFTTYADNQPAVTJOVFEGERALTKD
SQADIDRALSBAFKYAEEDERHRGRIAARNQLETVLFGVKEAAENGGDTAANNITIKNDKGGL
SQADIDRALSBAFKYAEEDERHRGRIAARNQLETVLFGVKEAAENGGDTAADKSSI
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            GYKGPTVEEVD"
a 744 c
                                                     VERCSEAMKWLDSNTTAEKEEYEYKLKELEQFCSPIMTKMHKGGGDGQQAPNFGQQAG
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<1157. .>3064
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/db_xref="taxon:7227"
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32.4%; Pred. No. 12;
tive 23; Mismatches
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Li, L., Zhang, L.,

Beijing

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Drosophila melanogaster,
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Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 27067)
Adams, M. and Venter, J.C.
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HTG; HTGS_PHASE2
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For more information on this record e-mail to
FOR NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (30-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
24; Conserv
                                                                             Wang, J., Hu, S., Dong, W., Zhang, X., Wang, X., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Y., Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H., Liu, Y., Li, G., Li, C., Bao, Q., Bao, J., Wang, X., Song, L., Zhang, L., Guo, D., Huang, F., Zhang, G., Li, J., Bian, X., Zhang, M., Li, L., Feng, X., Yu, J. and Yang, H.
                                                                                                                                                                                                                                                                                ACO22005 165821 bp DNA HTG 03-FEB-2000 HOMO sapiens chromosome 3p clone RP11-378N17, WORKING DRAFT SEQUENCE, 19 unordered pieces.
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia;
Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (Dases 1 to 165821)
                                                                                                                                                                                                                                         HTG; HTGS_PHASE1; HTGS_DRAFT
                                                                                                                                                                                                                                                     AC022005.1 GI:6742900
Wang, J., Hu, S., Dong, W., Zhang, X., Wang, X., Zhang, Y., Zhang, H., Liu, B., Bao, W., Sun, Y., Wu, Q., Wang, H., Yang, X., Cheng, C., Wang, Niu, Y., Qi, X., Li, T., Zhang, H., Liu, N., Wu, D., Yu, B., Fan, H.,
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                                         (bases 1 to 165821)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="prosophila melanogaster"
/ob_xref="taxon:7227"
/db_xref="taxon:7227"
5994 c 5686 g 7574 t
                                                                      3p genomic sequence
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%; Pred. No. 23;
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NOTE: This is a 'working draft' sequence. It currently
NOTE: This is a 'working draft' sequence. It currently
consists of 19 contigs. The true order of the pieces
is not known and their order in this sequence record is
arbitrary. Gaps between the contigs are represented as
runs of N, but the exact sizes of the gaps are unknown.
This record will be updated with the finished sequence
as soon as it is available and the accession number will
be preserved.
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                            Direct Submission
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Adams, M.D., Celniker, S.E.,
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∕gene="CG5933"
                                                                                                  'chromosome-"3R"
                                                                                                                            /organism="Drosophila melanogaster"
/db_xref="taxon:7227"
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EBITI PANVTPEQVPTSIVDFSAVEQSEDALAAEINKAHVVCIVYAVDDDDTLDRITS
HWLPLVRAKCNESLDGECDAEAEAEGOTQREDIRKPIVLVGKKIDLIEYSTMDSVLAI
MEDYPELESCYCECSAKSLHVISEMFYYAQKAVLHFTSPLYMAEGDELTSACKKSLVRI
FKICDIDGDNLLNDYELNLFQRRCFNVFLQPQLLDEVKAVLQKNVPDGIYUDAVTLKG
FLFLCLFIQRGRNETTWAVLARFGYNDQLEMCQEYLRPPLKIPPGSSTELSHRGQQF
LIAVFERVENDEODGALSPEEKMLFSTCPAAPWSYSTDIRKSCPINSTTGWVTHGWL
VIGPKGSGKTOMCRGFLVEDMHKLIGKEFKTNVVNCINSVQVYGQEKHLILMDIDVRH
ALDPLOPGEWNCDVACLVYDSSNPRSFEYVARIYIKYAAESKIPVMIVGTKCDMDERR
ALDPLOPGEWNCDVACLVYDSSNPRSFEYVARIYIKYAESKIPVMIVGTKCDMDERR
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/db_xref="FLYBASE:FBgn0039141"
<15341. .>18742
                                          /protein_id="AAF56223.1"
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JOIN(15341. 16477,16713. 16883,17029. 17

17686. 17993,17997. 18742)

/gene="CG5977"
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                                                                                                                                                                                            /gene="CG597
                                                                                                               db_xref="FLYBASE:FBan0005977"
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/protein_id="AAF56222.1"
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/db_xref="FLYBASE:FBan0039140"
complement(join(12728. .13936,14049. .14666))
/gene="CG5410"
/note="CG5410 gene product"
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/db_xref="FLYBASE:FBgn0039139"
/protein_id="AAF56221.1"
/db_xref="GI:7301087"
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/db_xref="FLYBASE:FBan0005933"
/db_xref="FLYBASE:FBgn0039139"
<9315. .>11271
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/db_xref="FLYBASE:FBgn0039139"
/oin(9315. .9453,9516. .9809,9878.
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/db_xref="FLYBASE:FBgn0005649"
complement(join(21082. .21245, 22556. .23606,25079. .>25144))
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/gene="Rox8"
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/db_xref="FLYBASE:FBgn0005649"
complement(join(21082. .21245,21315.
22556. .22783))
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(join(21082. .21245,21315. .21408,21476. .22556. .22783))
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                                                                                                                                                           23.8%;
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                                                                                                                                                               Score 30.2;
Pred. No. 19;
                                                                                                                                     Mismatches
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                                                                                                                                                                                                      DB 34;
                                                                                                                                           13;
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/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="14"

RESULT 12

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source
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fruit fly.
Droco--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.

1 (bases 1 to 33556)
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* NOTE: This is a 'working draft' sequence.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence was identified as CDM:10213304 by the submitter. For more information on this record e-mail to flyecelera.com.
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                                                                                                                                                                                                                                                                                                                                                                                   CNSOIDV7 210788 bp DNA PRI 31-MAR-2000 Human chromosome 14 DNA sequence *** IN PROGRESS *** BAC R-1070N10 of RPCI-11 library from chromosome 14 of Homo sapiens (Human),
                                                  Submitted (31-MAR-2000) to the EMBL/GenBank/DDBJ databases on Apr 3, 2000 this sequence version replaced gi:6981914. On Apr 3, 2000 this sequence is unfinished and does not necessarly IMPORTANT: This sequence is unfinished and does not necessarly represent the correct sequence. Work on the sequence in progress and the release of this data is based on the understanding that the sequence may change as work continue. The sequence may be contaminated with foreign sequence from E.coli, yeast, vector,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 210788)
                                                                                                                                                                                                                                                                                                                                  AL133467.2 GI:7406475
                                                                                                                                                                                                                                                                                                                                                                   complete sequence.
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/db_xref="taxon:7227"
7236 c 7072 g 9750 t
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Pred. No.
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Drosophila melanogaster

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;

Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                              Drosophila melanogaster genomic scaffold of 30, complete sequence.
AE003489 AE002593
AE003489.1 GI:7207757
1 (bases 1 to 302915)
Adams, M.D., Celniker.S.E., Holt, R.A., Evans, C.A., Goca
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1 48476 c 50053 g 56515 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="matching EMBL:R70888; RHdb:RH77821; dbSTS:STS54563; Identified using the e-PCR software (G. Schuler)"
190705. .190868
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/10576-"matching EMBL:T72567; RHdb:RH44140; RHdb:RH1627;
dbSTS:STS4726; Identified using the e-PCR software (G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="matching EMBL:T96687; RHdb:RH45537; dbSTS:STS38605;
Identified using the e-PCR software (G. Schuler)"
189245. 189443
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dbsTS:STS66733; Identified using the e-PCR software
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/clone="R-1070N10"
11396. .11567
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 Gocayne, J.D.,
.A., Galle, R.F.,
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Benos, P. V. Berman, B. P. Bhandari, D. Bolshakov, S. Borkova, D.
Botchan, M. R. Bouck, J. Brokstein, P. Botthier, P. Burtis, K.C.
Cherry, J. Buytath, Cadleu, E. Center, A., Chandra, I.
Pablos, B. Butler, H. Cadleu, E. Center, A., Chandra, I.
Pablos, B. Delcher, A., Deng, Z. Mays, A. D., Dew, I. Davies, P., de
Dodson, K., Doup, L. E. Downess M. Dugan-Rocha, S., Dunkov, B.C.
Pleischmann, W., Fosler, C., Gabrielian, E., Garg, N. S.,
Gunn, P., Durbin, K. J. Evangelista, C.C., Ferraz, C., Ferrieras, S.,
Gunn, P., Harris, M., Harris, N. L. Harvey, D. Heiman, T. J.,
Wei, M. H. Ibgwam, C. Jalali, M., Kalush, F., Karpen, G.H., Ke, Z.,
Kravitz, S. Kulp, D. Lai, Z., Lasko, P. Lei, Y. Levitsky, A. A.,
McIeod, M. P., McPherson, D., Merkulov, G., Milshina, N. V., Mobstry, C.,
Morris, J. Moshrefi, A., Mount, S. M., Nelson, K. A., Nixon, K.,
Pollard, J., Puri, V., Reese, M.G., Reiner, K. N., Nixon, K.,
Sunders, R. D., Scheeler, F., Shen, H., Shue, B.C., Siden-Kiamos, I.,
Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C.,
Weinstock, G. M., Palazzolo, M., Pitman, G. S., Pan, S.,
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Stapleton, M., Strong, R., Sun, E., Svirskas, R., Tector, C., Turner, R.,
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Stapleton, M., Skupski, M. P., Smith, T., Spier, E., Spradling, A. C.,
Venter, E., Wang, A. H., Wang, Z. Y., Wassarman, D. A.,
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Bong, R. A., Wang, Z. Y., Wassarman, D. A.,
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Thong, W. Zhou, X., Zhang, G., Zhao, O., Zheng, Y. Heng, Y. H.,
Brith, H., O., Jang, G., Zhao, O., Zhang, L., Zheng, X. H.,
Theng, G. Shan, G. Shan, G. Shu, X., Smith, H.O.,
Theng, G. Shan, M. Shu, S., Zhan, Y. Shu, X., Smith, H.O.,
Theng, G. Shan, M. Shu, S., Zhan, Y. Shu, X., Shu, M. Shu, Zhu, X., Shu
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Submitted (21-MAR-2000) Celera Genomics, 45 West Gude Drive,
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                                    EU Arabidopsis
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200798 AATGATGTGTACACCCTCCTCGGTGAAACTGTAACGCTTGGGCGTGGATTGAGAGTCCTG 200857
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Arabidopsis thaliana DNA
AL132977
                                                                                                     Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
euhiophytes; Spermatophyta; Magnoliophyta; eudicotyledons; Core
eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae;
                                       1 (bases 1 to 109016)
Benes, V., Wurmbach, E., D
Lemcke, K., Mayer, K.F.X.,
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sequencing, project
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                                                  Drzonek,H., i
., Quetier,F.
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3, BAC c
                                                   Ansorge, W., Mewes, H.W., and Salanoubat, M.
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clone T10K17.
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	CDS	gene		exon	misc_feature	exon	intron	exon) in the case of t	- - - - - - - - -	exon	intron	exon	intron	. 6	9	intron								CDS	exon	!	gene	misc_feature			FEATURES Source	COMMENT	~~		JOURNAL	
	141511928,1204812130;1230812348,12502.		/gene-"T10K17.20"	•		complement (5855, 6400)	complement(57835854)	complement(56695782) /number=5	complement(55785668) /number=4	/number=4		complement(4375, .5511)	complement (4306 4374)	complement(41584305)	complement(40864157) /number=2	/number=1	GLNQPVWGREEDQAHGNDNSNLMAVSENVMVASANLHPNQVKMEL"	RIDFNLDTILASENGSLMDGSFNAAPMOLAWPOOAIETEOSFTHEOLOGDSTOOMS	ENQIPONOMINANGKAKDFEKKGKSSTKKNKSSEENEKLPYVHVRARRGOATDSHSLA	GGSTTALLELPTTQAVCTLLHFTDSSSSQQAAVTGIGGEIPPLHSFGGTLAFPSNSVL	/dp_xref="GI:6729523"	<pre>/product="putative protein" /protein_id="CAB67608.1"</pre>	/codon_start=1	/note="similarity to several hypothetical proteins -	complement(join(31133385,40864157,43064374, 55125577,56695782 5855 6400.	complement(31133385) /number=1		~ .		b1a" :3702"	organism="Arabidopsis thaliana"	<pre>ind 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/. Location/qualifiers 1. 100016</pre>	Information on performance of analysis and a more detailed	aston Cremieux, BP191, 91006 Evry Cedex, France;	lemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de project Coordinator: Marcel Salanoubat and Francis Quetier, Groupement	Submitted (19-JAN-1999) MIPS, at the Max-Planck-Institut fuer Blochemie, Am Klopferspitz 18a, D-82152 Martingtical Fac Total	Direct Submission
							CDS		exon	gene	exon	intron	- 6X01							CDS	gene		exon		intron	exon		intron	exon		intron	exon		3.			
FAGNSELCGFPLOKICK VITVSLISGVSIVIGAVS; NDEGFELEBDLRASA, DATWRRKDFENEVEAIS NTLPSLSWPERLLIAQG TRLVSGVSKLIGSLSAII CDVYSFGVVLMELLIGR	NFSKPVPTRLFNAVNLR TQLGSLVGTLNLSYNSF	ZΘ	/protein_id="CAB6 /db_xref="GI:6729	/product="recepto	<u>;</u>	T10K1 Stron	join(14857161)	/gene="T10K17.40	/gene="T10K17.40	/number=2 14857. 17399	complement(13803	complement(13529	complement(13360 /number=1	RKRIHVLVEHVQQSRC	/db_xref="GI:672	/product-"putati	/codon_start=1	RIBOSOMAL PROTEI	<pre>/note="ESTs matc any gene models</pre>	<pre>/gene="TIOK17.30 complement(join(</pre>	1336013903	/gene="T10K17.20		/gene="T10K17.2	/gene="IIOK1/.2 /number=4 12601 12710		/gene="T10K17.2		1230812348 /gene="T10K17.2			/number=1 1204812130 /gene="T10K17.2	/gene="T10K17.2	FDTYVRQIRDPHVWC IRVLYHGFGHYDALI	IESNMRNLYCYSRFA GKRVYTDYSIIAHGF	/translation="]	

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20" 20 4 20" 20" 20, 20" 207

30" 1(13360. .13528,13803. .13903)) Iching in this region do not correspond to s eg.GB:AA651588; similarity to 60S EIN L21 - Arabidopsis thaliana,

tive protein" NB67610.1" 729525" HIVNIPLMSPTTTVPDGIHTGSKOAYPSFTFGLKWVYQIGDKII KCAVEFKLRKKKNDELKAASKARGETISTKR"

3. .13903) 9. .13802)

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16196. .16749
/gene-"T10K17.40"
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Copyright (c) 1993 - 2000 Comp
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Porcine retrovirus
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Fowlpox virus (FPV
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ALIGNMENTS

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     V63778 standard: DNA: 940 BP. V63778; 17-MAR-1999 (first entry) Sequence derived from the 5' end Reticuloendotheliosis virus type
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Claim 6; Page 32; 43pp; French.

The present sequence is derived from the 5' end of the genomic RNA of RetLouLoendotheliosis virus type A (REV-A). The specification also of the genomic RNA of a type C retrovirus other than Friend murine leukaemia virus (FMLV) and Moloney murine leukaemia virus (HOMLV). The in a vector for permitting or enhancing the encapsidation of a retroviral vector. The vectors can be used for gene therapy, production of recombinant polypeptides or production of transgenic animals.

Sequence 578 BP; 94 A; 139 C; 172 G; 173 U;
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28-APR-1997; FR-005203.
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DARLIX JL, Gabus Darlix C, Lopez LM;
WPI; 99-037487/04.
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Sequence derived from the 5' end of REV-A.
Reticuloendotheliosis virus type A; REV-A;
type C retrovirus; internal ribosome entry
retroviral vector; gene therapy; ss.
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Pred. No. 2.4e-33;
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     REV-A.
REV-A; 5'
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site; IRES; encapsi
end genomic RNA;
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Se Reticule-ndotheliosis virus.

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         claim 18; Fig 6; 127pp; English.

Claim 18; Fig 6; 127pp; English.

The invention relates to a recombinant fowlpox virus (FPV) whose nucleic many invention relates to a recombinant fowlpox virus (REV), and acid does not encode an active reticuloendotheliosis virus (REV), and acid does not encode against fowlpox virus. The recombinant FPV is whose genome does not contain any REV sequence. The recombinant FPV is used to produce a vaccine against fowlpox virus. The vaccine is used to prevent the occurrence of fowlpox virus in chickens. The chickens can be prevent than 1 day of age. Alternatively, chickens older than naccinated at older than 1 day of age. Prior vaccine and field strains fev M (FPV mild strain) at 1 day of age. Prior vaccine and field strains of FPV carry integrated REV sequences. Some of the FPV strains carry a near full length provirus of REV, and can give rise to infectious REV when transfected into cell cultures and when chickens are infected. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Powlpox virus (FPV S) 5' ITR sequence.
Fowlpox virus; FPV; recombinant; reticuloendotheliosis virus;
vaccine; chicken; LTR; long terminal repeat; ss.
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08-AUG-1997; AU-008454.
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W09907852-Al
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (CSIR) COMMONWEALTH SCI & J
Boyle DB, Coupar BEH, Gould
WPI; 99-167428/14.
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R Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect mability to produce proyerus

T host cell and form provirus

Example; Page 16-17; 28pp; English.

Example; Page 16-17; Page 16-17; 28pp; English.

Example; Page 16-17; 28pp; English.

Examp
                                                                                                                                                                   Query Match
Best Local
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Q76040;
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Retrovirus: vector
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WPI; 95-0364
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  1216
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US-073345.
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Pred. No. 1.5e
36; Mismatches
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                                                                                                                                                           Score 116.6;
Pred. No. 1.3e
33; Mismatches
                                                                                                                                                                                116.6;
No. 1.
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Or 5039 standard; DNA, John AC 076039; (first entry)
DE 20-JUL-1995 (first entry)
DE Retrovirus vector pp0111-R2; spleen necrosis virus; SNV;
Retrovirus; CMV; intermediate-early promoter; IE proving terminal repeat; LTR; encapsidation; gene transfer;
SN 10ng terminal repeat; LTR; encapsidation; gene transfer;
SN 20ne therapy; ss.
Spleen necrosis virus.
Spleen necrosis virus.
PN 009429437-A.
PN 009429437-A.
PN 07-JUN-1994; U06415.
PR 07-JUN-1994; U06415.
PR 07-JUN-1994; U07-1994; U0
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Recombinant retrovirus vector, contg. ability to produce progeny virus, in host cell and form provirus Example; Page 13-14; 28pp; English. New recombination-free, highly efficippOll1-R1 (given in 076038), pPOll1-I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TRECOMBINANT retrovirus vector, contg. non-retroviral gene, has realisty to produce progeny virus, in helper cell which can infect both control of the left sex recombination-free, highly efficient retroviral vectors (PPO111-R1 (given in 076038), pPO111-R2 (076039) and pPO111-R3 (Q76040) were obtained by replacing the U3 region of the left CIR of spleen necrosis virus with the IE promoter/enhancer of cell-type specific gene expression and eliminate risks of downstream activation of cellular proto-oncogenes.

Sequence 5525 BP; 1264 A; 1422 C; 1457 G; 1382 T;
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Best Local Similarity 69.9
Matches 86; Conservative
                                                                                                                                                                                                                                                                               Q76038;
20-JUL-1995 (first entry)
20-JUL-1995 (first entry)
Retrovirus vector pPO111-R1.
Retrovirus; vector; pPO111-R1, spleen necrosis virus; SNV;
Cytomegalovirus; CMV; intermediate early promoter; IE prom
'\^^ +=rminal repeat; LTR; encapsidation; gene transfer;
                                                                                                                                  Dornburg RC;
WPI; 95-036467/05.
                                                                                                                                                                        22-DEC-1994, U06415, 07-JUN-1994, US-073345, US-073345, UNIV NEW JERSEY.
                                                                                                                                                                                                                                                           long terminal repeat;
gene therapy; ss.
Spleen necrosis virus.
W09429437-A.
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Q76038;
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69.9%;
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  ly efficient retroviral pPO111-R2 (Q76039) and
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Pred. No. 1.3e-29;
3; Mismatches 4
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us, in

    non-retroviral gene,
    helper cell which can

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88888
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Best Local s
Matches 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Retrovirus vector pPol15-R1; s; Retrovirus vector; pPol15-R1; s; gene transfer; gene therapy; ss. Spleen necrosis virus. W09429437-A. 22-DEC-1994; U06415. 07-JUN-1994; U06415. 07-JUN-1994; U07-JUN-1994; U07-JUN-1
                                                                                                                                                                                                                                                                                                   1213
                                                                                                                                                                                                                                                                                                                                                                                         Recombinant retrovirus vector, contg. non-retroviral gene, - has ability to produce progeny virus, in helper cell which can infect host cell and form provirus

bast cell and form provirus

Example; Page 17; 28pp; English.

The universal retroviral vector pp0115-R1 (given in 076041) was obtained by replacing the SV40 promoter and hpt gene of pp0111-R1 (276038) with the multiple cloning site of pBluescript II KS. The of downstream activation of cellular proto-oncogenes.

Sequence 3878 BP; 922 A; 948 C; 988 G; 1020 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 95-036467/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q76041;
Q76041;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dornburg RC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1285
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121
                                                                                                                                                                                                                                                        standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83;
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                                           (first entry)
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                                                                                                               DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          89.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         : Score 113.6; DB :
: Pred. No. 1.1e-28;
33; Mismatches 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ВP
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Pred. No. 1.3e-29;
3; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               spleen necrosis virus; SNV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4.
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Human mcl-1 Myeloid cel

cell

leukemia-associated

gene;

mcl-1; diagnostic;

gene

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Best Local S
Matches 27
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22-DEC-1994.
21-MAR-1994; U03547.
16-JUN-1993; US-0778
(UYJO) UNIV JOHNS I
                                                                                                                                                                                                                                                                                                             02-NOV-1994; AT-002038.
(BIOM-) BIOMAY PRODN & HANDEL:
Achatz G. Breitenbach M. Ebr
Oberkofler H. Prillinger H. S
WPI; 96-040555/05.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New myeloid cell leukaemia associated gene mcl-1 - used to develop prods. for detection and treatment of cell proliferative disorders, partic. myeloid cell leukaemia disorders, page 46-49; 67pp; English. Disclosure; Page 46-49; 67pp; English. DNA encoding new myeloid cell leukemia associated gene mcl-1 was 100 and 100 arms prepd. from ML-1 human myeloblastic isolated from a CDNA library prepd. from ML-1 human myeloblastic leukemia cells induced with TPA. The predicted gene product (given in R68814) contained 350 amino acids and had a mol.wt. of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_difference
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Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               p-PSDB; R68814.
New myeloid cell leukaemia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craig RW;
WPI; 95-036391/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1996 (first entry)
Allergen Alt a 12 protein encoding cDNA.
Alt a 45; Alt a 12; allergen; epitope; immunoglobulin detection; immunotolerance; anergy; ds.
Alternaria alternata.
                                                                                                                      r-rsus; Roouya.

Recombinant DNA encoding allergens of Alternaria alternata - useful Recombinant DNA encoding allergens of Alternaria alternata alternata in diagnosis and treatment of A. alternaria alternaria sequence encodes an Alt a 12 allergen protein isolated from The present sequence encodes an Alt a 12 allergen protein isolated from Alternaria alternata. Peptide epitopes from Alt a 12 and Alt a 45 Alternaria alternata. Peptide epitopes from Alt a 12 and For in vitro detection (R88672) are useful as diagnostic reagents, e.g. for in vitro detection (R88672) are useful as diagnostic reagents, e.g. for in vitro detection for allergy caused by Alt a 45 and 12 (by reaction with IgE in serum). The peptides of allergy can also detect cellular reaction to the specified allergens (from They can also detect cellular reaction to the specified allergens (their stimulatory or inhibitory effect on this reaction). The peptides can also be used therapeutically to induce immunotolerance or anergy of
                                                                                     r lymphocytes.
                                                                                                                                                                                                                                                                                                  P-PSDB; R88692
                                                                                                                                                                                                                                                                                                                                                                                                             02-NOV-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                             AT9402038-A.
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l Similarity 56.2%;
27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3946 BP;
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US-077848.
21.6%;
nilarity 47.5%;
Conservative 1
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M, Ebner C, K
er H, Simon B,
                                                                                             66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mRNA;
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       Score 27.4; DB Pred. No. 2.2; 11; Mismatches
                                                                                             101
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Unger
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                                                                                                                                                                                                                                                                                                                                                                     Lechenauer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pr New epidermal surface antigen and DNA encoding it - are useful to private the diseases such as cancer, and to detect restriction fragment private the polymorphisms on human chromosome 17 associated with private 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                밁
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Best Local Similarity
Matches 20; Conserv
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14-APR-1994; U09309.
30-SEP-1993; US-956841.
01-OCT-1992; US-956841.
(TEXA ) UNIV TEXAS SYSTEM.
CUPYIC M, SCHOOGER WT;
WPT; 94-135503/16.
P-PSDB; R51108.
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epidermal surface antigen; human chromosome 17; cancer; RFLP; epidermal surface antigen; human chromosome 17; cancer; RFLP; epidermal surface antigen; human chromosome 17; cancer; Restriction fragment length polymorphism; autoimmune bullous disportants; Recklinghausen neurofibromatosis; NF1 locus; psoriasis; NF1 locus; NF1 locus; NF1 locus; psoriasis; NF1 locus; NF1 locus; psoriasis; NF1 locus; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q45332 standard;
Q45332;
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    gene therapy; probe; (
Homo sapiens.
US5691460-A.
25-NOV-1997.
22-JUL-1994; 279270.
22-JUL-1994; US-279270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     foliaceus; ss.
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                                                                                                                                                                                                                                            27-MAR'1998 (first entry)
DNA for epidermal surface antigen.
DNA for epidermal surface antigen; treatment; diagnosis;
Epidermal surface antigen; treatment; diagnosis;
autolmmune bullous disease; pemphigus; bullous pemphigoid;
autolmmune bullous disease; pemphigus; bullous pemphigoid;
gene therapy; probe; detection; chromosome 17 abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                T95887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           T95887;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; DNA;
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                        US-279270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers 127. .1002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CDNA;
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/product= surface_antigen
/transl_except= pos:259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.3%;
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Pred. No. 5.3;
13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5.3;
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Pr Nucleic acid encoding human aminopeptidase p
Claim 13; Page 109-139; 201pp; English.

CC This invention describes the isolation of a novel human aminopeptidase p
CC (Amp). This protein is used to produce recombinant Amp and can be used
CC for gene therapy for treating Amp-deficiency conditions, Its fragments
CC are used as primers and probes to identify patients with homozygous and
CC defective in Amp are at risk of developing angioedema if treated with
CC in cases of excessive Amp expression. The product of the invention is
CC generate transgenic animals, and comparisons of genomic sequences are
CC used to detect mutations. Amp inhibitors are potentially useful as
CC or atheroscierosis. The structure of Amp is used to design synthetic
CC inido bonds, can be used to degrade industrial protein feeds to free
CC amino acids, to degrade proteinaceous wastes, as additives in enzyme
CC methods to study Amp distribution.
S0 Sequence 4998 BP; 12805 A; 11725 C; 11351 G; 14317 T;
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                                                 Query Match
Best Local S
Matches 26
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human kidney aminopeptidase p genomic DNA fragment 2. Aminopeptidase; human; AmP; gene therapy; treatment; AmP-deficiency; prenatal diagnosis; angioedema; antihypertensive agent; atherosclerosis; arterial stenosis; industrial protein feed; malabsorption syndrome; proteinaceous waste degradation; additive; immunohistochemistry; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     Ryan Jw, Sprinkle TJC, Venema
                                                                                                                                                                                                                                                                                                                                                                                                                  02-SEP-1998; U18426.
02-SEP-1997; US-057854.
(MEDI-) MEDICAL COLLEGE GEORGIA RES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
WO9911799-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  X23518 standard; DNA; 49998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-OCT-1992; US-956841.
(TEXA ) UNIV TEXAS SYSTEM.
DUV1C M, Schroeder WT;
WPI; 98-017714/02.
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                                                           Similarity
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nilarity 46.5%;
Conservative 1
                                              19;
                                        Score 27; DB
Pred. No. 12;
19; Mismatches
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                                                     DB
12;
                                        30;
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                                        Indels
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                                      Gaps
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CTGCAGTGGGCAGTGCCCTCCCCACCTGGCTGGCGGCCCAGGCATTGCTGCCTCTTTCCA 960 cugcgaauuggugugcccacaccgcgcgcggcuugcgaauaauacuuuggagagucuuuugc 73

901

14

Similarity

Conservative

16;

. 9 DB 52;

Length 1760; Indels

0

Gaps

0;

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Processing the solution of liver activin - provided including sub-units of liver activin - provided including growth and differentiation of cells, e.g. for useful for regulating growth and differentiation of cells, e.g. for provides marine liver activin beta e polypeptide. The invention CC provides marine liver activin beta c and beta e genes. Disorders of cell crowth or differentiation (or susceptibility to them) are diagnosed by activin gene. Disorders of haematopolesis, erythroid differentiation, compound secretion or cardiac covarian follicular maturation, hormone secretion or cardiac covariant follicular maturation, hormone secretion or cardiac covariant follicular maturation that can be diagnosed using the liver covariant follicular activin compound or agent that upregulates the compound's caponists can be used to increase growth and regeneration of liver tissue. Cc agonists can be used to increase growth and regeneration of liver tissue. Cc astroporosis or osteomalacia) or haematopolesis, particularly cultivincorders. Antibodies (which bind to liver activin receptors) and to consist the produce the liver activin correctly processed and cc screening for liver activin modulators.

Sequence 1760 BP; 390 A; 502 C; 514 G; 354 T;
                                                                                                         Query Match
Best Local S
Matches 42
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V38240
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20-NOV-1996; US-755919;
(UNMI) UNIV MICHIGAN.
Bonaddo J, Fang J;
WPI: 98-312408/27.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human liver activin beta e polypeptide encoding cDNA.
Liver activin; beta c; beta e; cell differentiation; haematopoiesis;
erythroid; ovarian follicular maturation; hormone; neuronal survival
spermatogenesis; bone; insulin; cardiac morphogenesis; osteoporosis;
osteomalacia; erythropoiesis; haemophilia; cystic fibrosis; immunoas;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sig_peptide
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V38240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             disorder; transgenic; modulator;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= ____
127. .1126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product-
77. .126
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                      21.1%; 38.2%;
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beta e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "activin beta e polypeptide"
Score 26.8; DI
Pred. No. 5.6;
16; Mismatches
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961 TICTGCCGTCTTCAGCCTCCTCAAAGCCAACAATCCTTGGCCTGCCAGTA 1010

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RESULT 15
Q70072
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                                                             pp N J06189766-A.

pp 12-JUL-1994.

pp 12-DEC-1992; 359265.

pr 25-DEC-1992; JP-359265.

pr 25-DEC-192; JP-359265.

pr 25-DEC
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Best Local Similarity 39.7
Matches 31; Conservative
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25-DEC-1992; 359265.
25-DEC-1992; JP-359265.
(TOFU ) TONEN CORP.
WPI; 94-259533/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New DNA sequence encoding canine zona pellucida CZP2 - useful for the prodn. of a canine contraceptive vaccine antigen Disclosure; Page 4-5; 10pp; Japanese. Disclosure; Page 4-5; 10pp; Japanese. The CZP2 DNA (070072) was prepd. by the cloning of CZP2(75-520) - Q81700 using the primers given in 070073-74, CZP2(1-65) - Q81804 using the primers given in 070082-83, CZP2(42-103) - Q81803 using the primers given in 070079-81 and CZP2(487-713) - Q81957 using the primers given in 070075-78. Sequence 1335 BP; 385 A; 331 C; 277 G; 342 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q81700 standard; cDNA to mRNA; 1335 BP Q81700;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antigen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Canine; dog; zona
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
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Canine zona pellucida CZP2.
Canine; dog; zona pellucida;
antigen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q70072 standard; cDNA to mRNA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2216 BP
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Length 2216;
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Query Match

20.68;

Score 26.2;

DB 1;

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Best Local Similarity 39.2 Matches 31; Conservative
             39.2%;
   ; Pred. No. 9.4;
15; Mismatches
       33,
        Indels
          0,
          Gaps
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QΥ 100 ccuccucucccucuccggc 118

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2000, 09:21:45

Search completed: August 7, Job time: 478 sec

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